



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 95546

TO: Jeffrey Parkin
Location: CM1 8E15
Art Unit: 1648
Thursday, June 05, 2003

Case Serial Number: 605573

From: Alex Waclawiw
Location: Biotech-Chem Library
CM1-6A02
Phone: 308-4491

Alexandra.waclawiw@uspto.gov

Search Notes

Examiner Parkin,

I was not able to remove the inventor's name from the compugen search. The program does not allow for that option.

I also searched the sequence on STN. There were no sequences with less than 20 amino acids. I printed out hits with sequence length between 20-30 amino acids just in case this information would be useful. The reference for these sequences was the inventor's work

Alexandra Waclawiw

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or contact:

Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library CM1 – Circ. Desk



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Parkin 09/605,573

=> dhis

(FILE 'HOME' ENTERED AT 10:54:21 ON 05 JUN 2003)

FILE 'REGISTRY' ENTERED AT 10:55:14 ON 05 JUN 2003
L1 16 S LNSWGCKGRIICYTS/SQSP
L2 0 S L1 AND SQL<21
L3 0 S L1 AND SQL=20
L4 9 S L1 AND SQL<31

FILE 'HCAPLUS' ENTERED AT 10:58:23 ON 05 JUN 2003
L5 1 S L4

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=> fil reg

FILE 'REGISTRY' ENTERED AT 10:58:51 ON 05 JUN 2003
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
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Property values tagged with IC are from the ZIC/VINITI data file
provided by InfoChem.

STRUCTURE FILE UPDATES: 4 JUN 2003 HIGHEST RN 525536-93-0
DICTIONARY FILE UPDATES: 4 JUN 2003 HIGHEST RN 525536-93-0

TSCA INFORMATION NOW CURRENT THROUGH JANUARY 6, 2003

Please note that search-term pricing does apply when
conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. See HELP
PROPERTIES for more information. See STNnote 27, Searching Properties
in the CAS Registry File, for complete details:
<http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf>

=> d que 14

L1 16 SEA FILE=REGISTRY ABB=ON PLU=ON LNSWGCKGRIICYTS/SQSP
L4 9 SEA FILE=REGISTRY ABB=ON PLU=ON L1 AND SQL<31

=> d sqide3 14 1-9

L4 ANSWER 1 OF 9 REGISTRY COPYRIGHT 2003 ACS
RN 276694-91-8 REGISTRY
CN L-Histidine, glycy-L-arginyl-L-.alpha.-glutamyl-L-threonyl-L-leucyl-L-
methionyl-L-glutaminyglycyl-L-glutaminy-L-glutaminy-L-phenylalanyl-L-
leucyl-L-asparaginy-L-seryl-L-tryptophylglycyl-L-cysteinyl-L-lysylglycyl-
L-arginyl-L-isoleucyl-L-isoleucyl-L-cysteinyl-L-tyrosyl-L-threonyl-L-seryl-
L-alanyl-L-arginyl-L-tryptophyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 4: PN: JP2000157268 PAGE: 37 claimed sequence
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 30

PATENT ANNOTATIONS (PNTE):

Sequence	Patent
Source	Reference
Not Given	JP2000157268
	claimed PAGE
	37

SEQ3 1 Gly-Arg-Glu-Thr-Leu-Met-Gln-Gly-Gln-Gln-
11 Phe-Leu-Asn-Ser-Trp-Gly-Cys-Lys-Gly-Arg-
=== ===
21 Ile-Ile-Cys-Tyr-Thr-Ser-Ala-Arg-Trp-His
=== ===

HITS AT: 12-26

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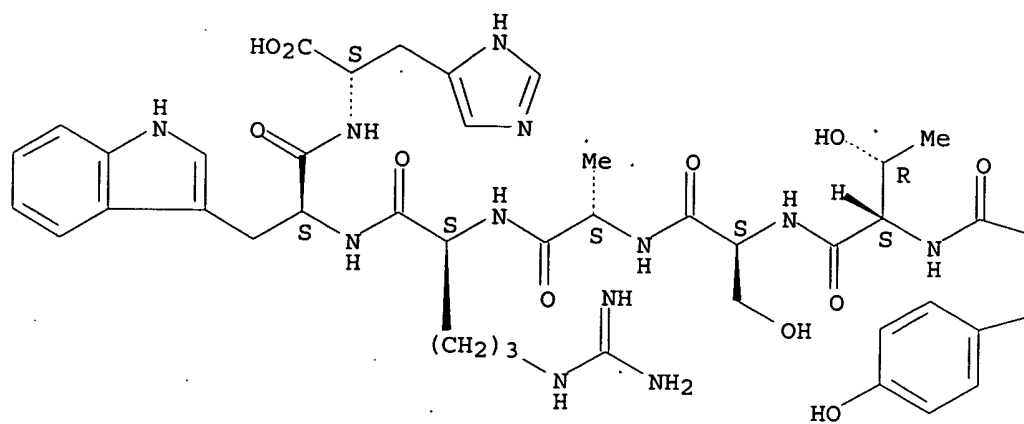
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SR CA

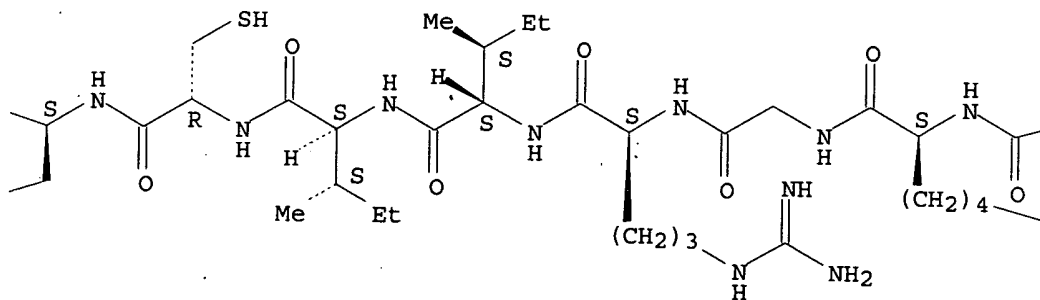
LC STN Files: CA, CAPLUS, USPATFULL

Absolute stereochemistry.

PAGE 1-A

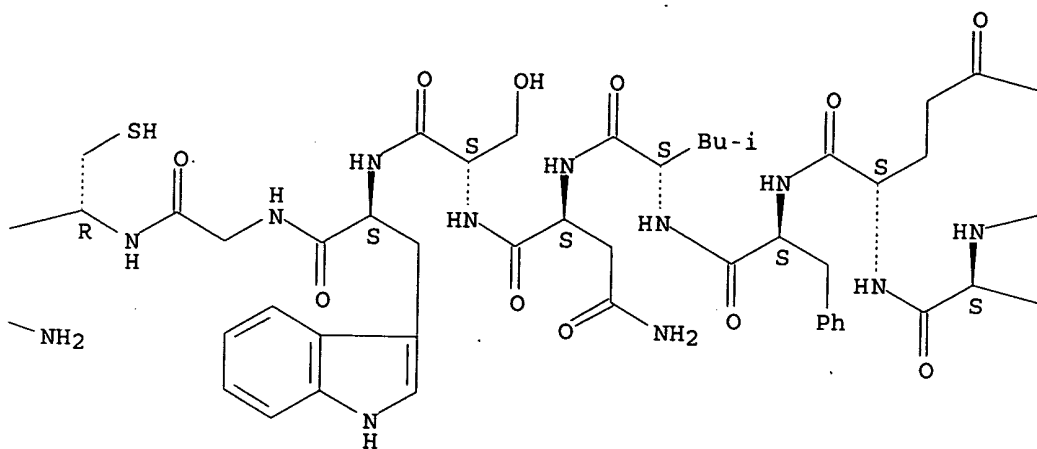


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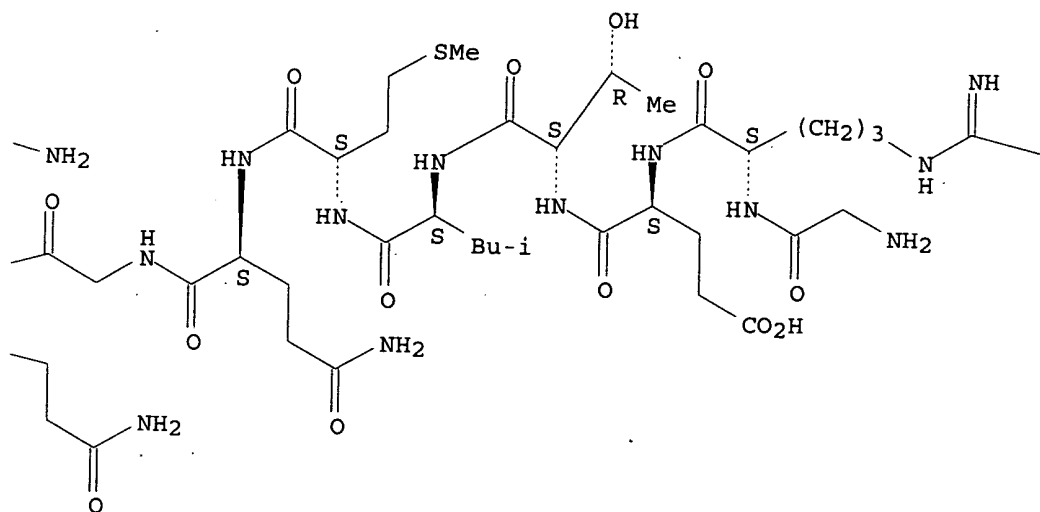


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PAGE 1-C



PAGE 1-D



PAGE 1-E

NH₂

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1 REFERENCES IN FILE CA (1957 TO DATE)
1 REFERENCES IN FILE CAPLUS (1957 TO DATE)

L4 ANSWER 2 OF 9 REGISTRY COPYRIGHT 2003 ACS
RN 276687-01-5 REGISTRY
CN Peptide, (Glu-Thr-Leu-Met-Gln-Xaa-Gln-Gln-Arg-Leu-Asn-Ser-Trp-Gly-Cys-Lys-Gly-Arg-Ile-Ile-Cys-Tyr-Thr-Ser-Ala-Arg-Trp-His) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 6: PN: JP2000157268 PAGE: 37 claimed sequence
FS PROTEIN SEQUENCE
SQL 28
NTE

type	location	description
uncommon	Aaa-6	

PATENT ANNOTATIONS (PNTE):

Sequence	Patent
Source	Reference
Not Given	JP2000157268 claimed PAGE 37

SEQ3 1 Glu-Thr-Leu-Met-Gln-Aaa-Gln-Gln-Arg-Leu-
11 Asn-Ser-Trp-Gly-Cys-Lys-Gly-Arg-Ile-Ile-
21 Cys-Tyr-Thr-Ser-Ala-Arg-Trp-His

HITS AT: 10-24

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, USPATFULL
1 REFERENCES IN FILE CA (1957 TO DATE)
1 REFERENCES IN FILE CAPLUS (1957 TO DATE)

L4 ANSWER 3 OF 9 REGISTRY COPYRIGHT 2003 ACS
RN 276687-00-4 REGISTRY
CN Peptide, (Xaa-Gln-Gln-Arg-Leu-Asn-Ser-Trp-Gly-Cys-Lys-Gly-Arg-Ile-Ile-Cys-Tyr-Thr-Ser-Ala-Arg-Trp-His) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 5: PN: JP2000157268 PAGE: 37 claimed sequence
FS PROTEIN SEQUENCE
SQL 23
NTE

type	location	description
uncommon	Aaa-1	

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PATENT ANNOTATIONS (PNTE):

Sequence	Patent
Source	Reference
=====	
Not Given	JP2000157268
	claimed PAGE
	37

SEQ3 1 Aaa-Gln-Gln-Arg-Leu-Asn-Ser-Trp-Gly-Cys-
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 11 Lys-Gly-Arg-Ile-Ile-Cys-Tyr-Thr-Ser-Ala-
 === === === === ===
 21 Arg-Trp-His

HITS AT: 5-19

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, USPATFULL

1 REFERENCES IN FILE CA (1957 TO DATE)

1 REFERENCES IN FILE CAPLUS (1957 TO DATE)

L4 ANSWER 4 OF 9 REGISTRY COPYRIGHT 2003 ACS

RN 276250-49-8 REGISTRY

CN 4: PN: JP2000157268 SEQID: 63 unclaimed protein (9CI) (CA INDEX NAME)

FS PROTEIN SEQUENCE

SQL 30

NTE

type	location	description
uncommon	Aaa-8	-

PATENT ANNOTATIONS (PNTE):

Sequence	Patent
Source	Reference
=====	
Not Given	JP2000157268
	unclaimed
	SEQID 63

SEQ3 1 Gly-Arg-Glu-Thr-Leu-Met-Gln-Aaa-Gln-Gln-
 11 Arg-Leu-Asn-Ser-Trp-Gly-Cys-Lys-Gly-Arg-
 === === === === ===
 21 Ile-Ile-Cys-Tyr-Thr-Ser-Ala-Arg-Trp-His
 === === === === ===

HITS AT: 12-26

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, USPATFULL

1 REFERENCES IN FILE CA (1957 TO DATE)

1 REFERENCES IN FILE CAPLUS (1957 TO DATE)

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L4 ANSWER 5 OF 9 REGISTRY COPYRIGHT 2003 ACS
RN 276250-48-7 REGISTRY
CN 3: PN: JP2000157268 SEQID: 62 unclaimed protein (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE
SQL 28
NTE

type	location	description
uncommon	Aaa-6	

PATENT ANNOTATIONS (PNTE):

Sequence | Patent

Source | Reference

=====+=====

Not Given	JP2000157268
	unclaimed
	SEQID 62

SEQ3 1 Glu-Thr-Leu-Met-Gln-Aaa-Gln-Gln-Arg-Leu-
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11 Asn-Ser-Trp-Gly-Cys-Lys-Gly-Arg-Ile-Ile-
=====
21 Cys-Tyr-Thr-Ser-Ala-Arg-Trp-His
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HITS AT: 10-24

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, USPATFULL

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1 REFERENCES IN FILE CAPLUS (1957 TO DATE)

L4 ANSWER 6 OF 9 REGISTRY COPYRIGHT 2003 ACS
RN 276250-47-6 REGISTRY
CN 2: PN: JP2000157268 SEQID: 60 unclaimed protein (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE
SQL 23
NTE

type	location	description
uncommon	Aaa-1	

PATENT ANNOTATIONS (PNTE):

Sequence | Patent

Source | Reference

=====+=====

Not Given	JP2000157268
	unclaimed
	SEQID 60

SEQ3 1 Aaa-Gln-Gln-Arg-Leu-Asn-Ser-Trp-Gly-Cys-

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11 Lys-Gly-Arg-Ile-Ile-Cys-Tyr-Thr-Ser-Ala-
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21 Arg-Trp-His

HITS AT: 5-19

****RELATED SEQUENCES AVAILABLE WITH SEQLINK****

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, USPATFULL

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1 REFERENCES IN FILE CAPLUS (1957 TO DATE)

L4 ANSWER 7 OF 9 REGISTRY COPYRIGHT 2003 ACS

RN 275801-53-1 REGISTRY

CN 135: PN: JP2000157268 SEQID: 69 unclaimed sequence (9CI) (CA INDEX NAME)

FS PROTEIN SEQUENCE; STEREOSEARCH

SQL 30

PATENT ANNOTATIONS (PNTE):

Sequence | Patent

Source | Reference

=====+=====

Not Given | JP2000157268

| unclaimed

| SEQID 69

SEQ3 1 Gly-Arg-Glu-Thr-Leu-Met-Gln-Asp-Gln-Gln-

11 Arg-Leu-Asn-Ser-Trp-Gly-Cys-Lys-Gly-Arg-

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=== === === === ===

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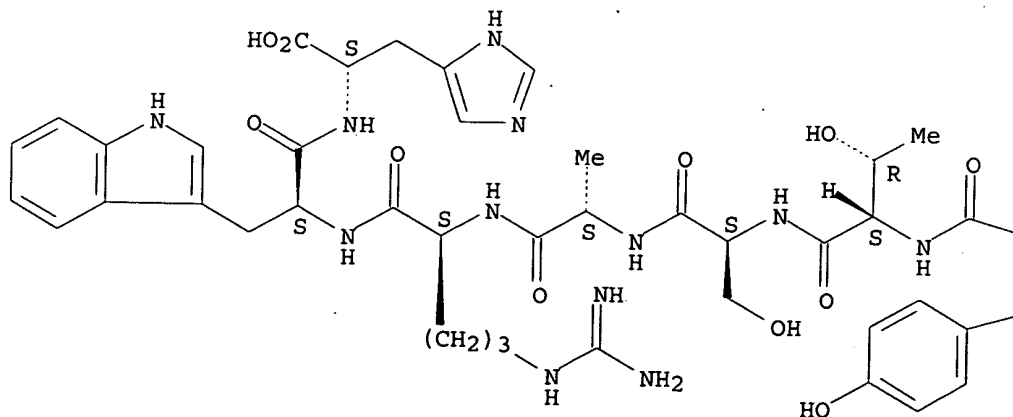
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LC STN Files: CA, CAPLUS, USPATFULL

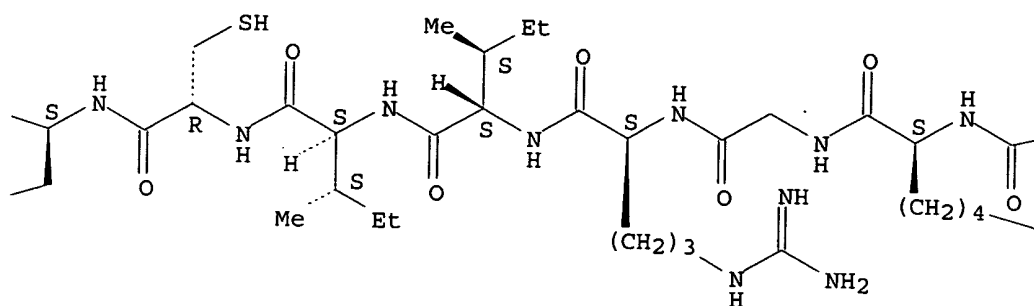
Absolute stereochemistry.

PAGE 1-A

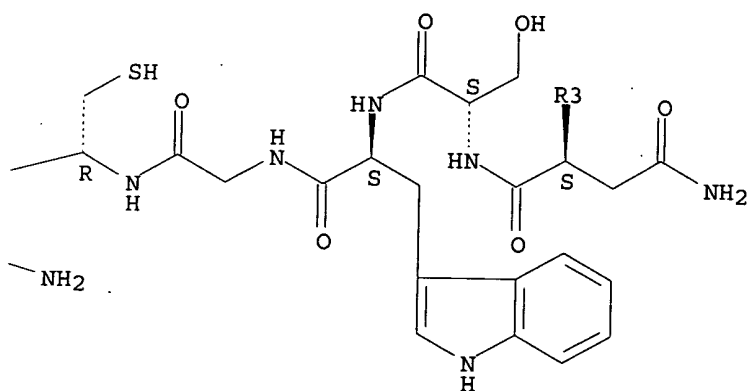


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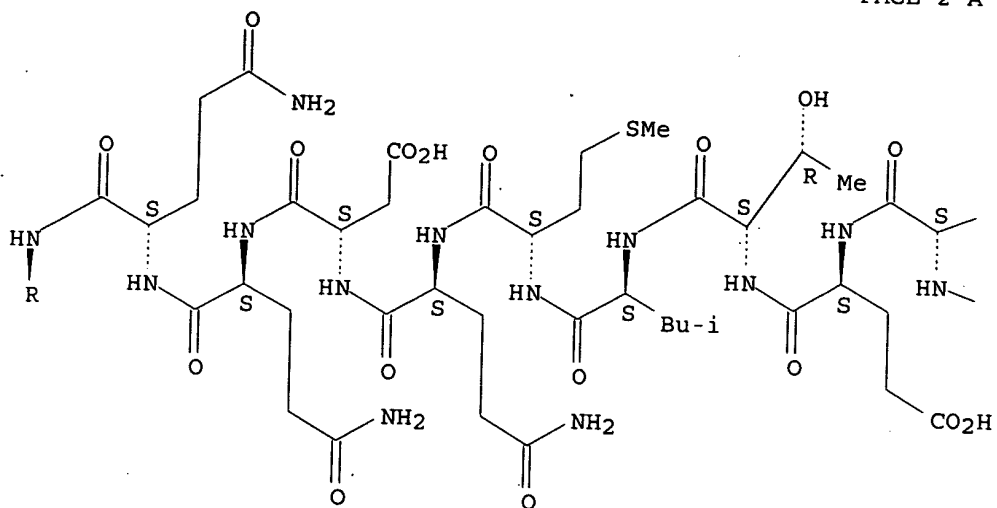


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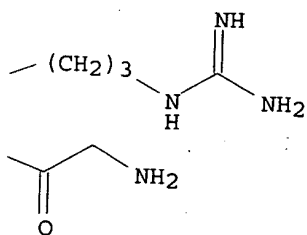


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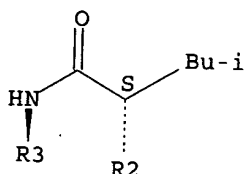
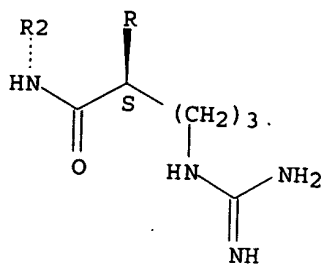
PAGE 2-A



PAGE 2-B



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1 REFERENCES IN FILE CA (1957 TO DATE)
1 REFERENCES IN FILE CAPLUS (1957 TO DATE)

L4 ANSWER 8 OF 9 REGISTRY COPYRIGHT 2003 ACS
RN 275801-51-9 REGISTRY
CN L-Histidine, L-.alpha.-glutamyl-L-glutaminyl-L-glutaminyl-L-arginyl-L-leucyl-L-asparaginy-L-seryl-L-tryptophylglycyl-L-cysteinyl-L-lysylglycyl-L-arginyl-L-isoleucyl-L-isoleucyl-L-cysteinyl-L-tyrosyl-L-threonyl-L-seryl-L-alanyl-L-arginyl-L-tryptophyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 127: PN: JP2000157268 SEQID: 61 unclaimed sequence
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 23

PATENT ANNOTATIONS (PNTE):

Sequence	Patent
Source	Reference
Not Given	JP2000157268
	unclaimed
	SEQID 61

SEQ3 1 Glu-Gln-Gln-Arg-Leu-Asn-Ser-Trp-Gly-Cys-
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11 Lys-Gly-Arg-Ile-Ile-Cys-Tyr-Thr-Ser-Ala-
=====
21 Arg-Trp-His

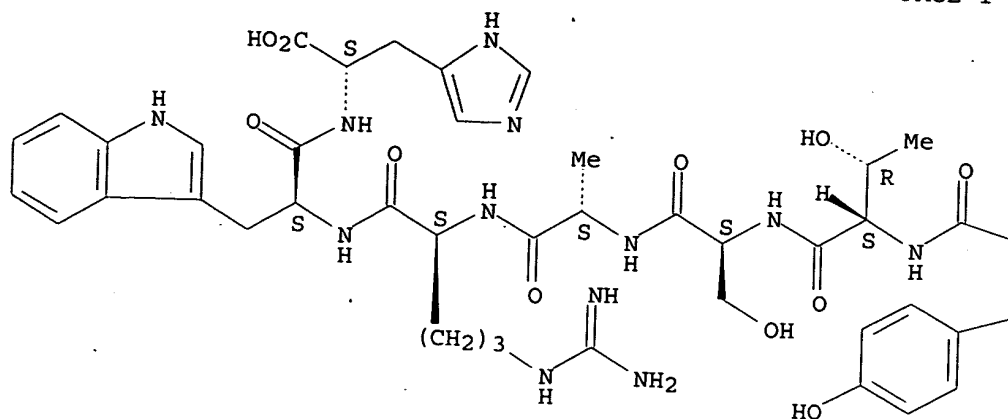
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LC STN Files: CA, CAPLUS, USPATFULL

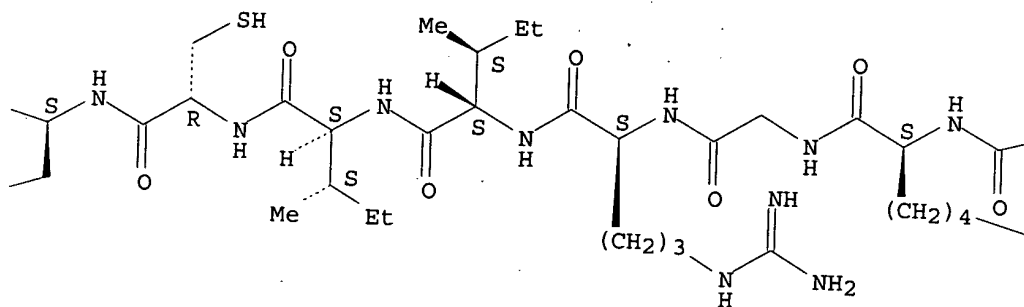
Absolute stereochemistry.

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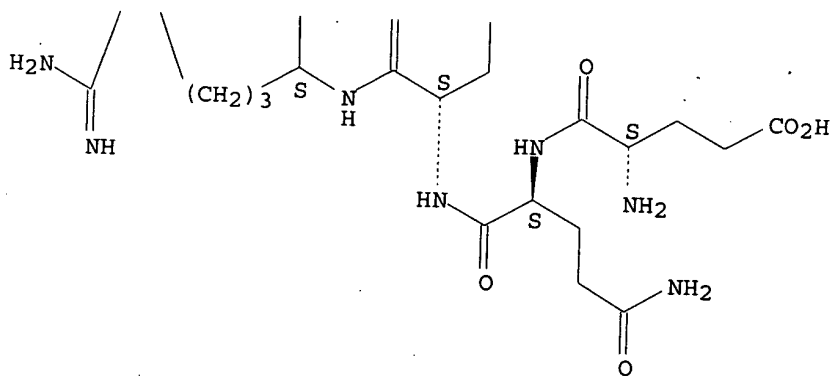
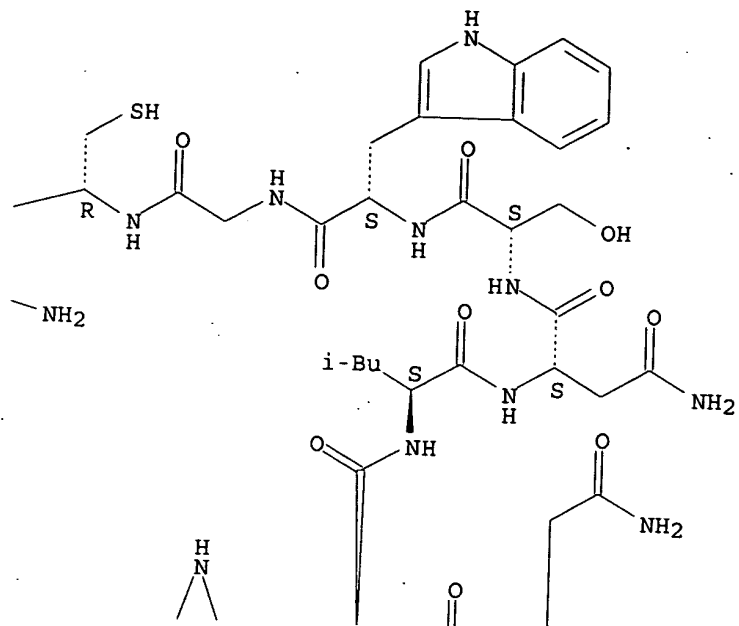
PAGE 1-A



PAGE 1-B



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1 REFERENCES IN FILE CAPLUS (1957 TO DATE)

L4 ANSWER 9 OF 9 REGISTRY COPYRIGHT 2003 ACS
RN 275801-47-3 REGISTRY
CN L-Histidine, L-asparaginyl-L-glutaminyl-L-glutaminyl-L-arginyl-L-leucyl-L-asparaginyl-L-seryl-L-tryptophylglycyl-L-cysteinyl-L-lysylglycyl-L-arginyl-L-isoleucyl-L-isoleucyl-L-cysteinyl-L-tyrosyl-L-threonyl-L-seryl-L-alanyl-L-arginyl-L-tryptophyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 125: PN: JP2000157268 SEQID: 59 unclaimed sequence
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 23

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PATENT ANNOTATIONS (PNTE):

Sequence	Patent
Source	Reference
Not Given	JP2000157268
	unclaimed
	SEQID 59

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 21 Arg-Trp-His

HITS AT: 5-19

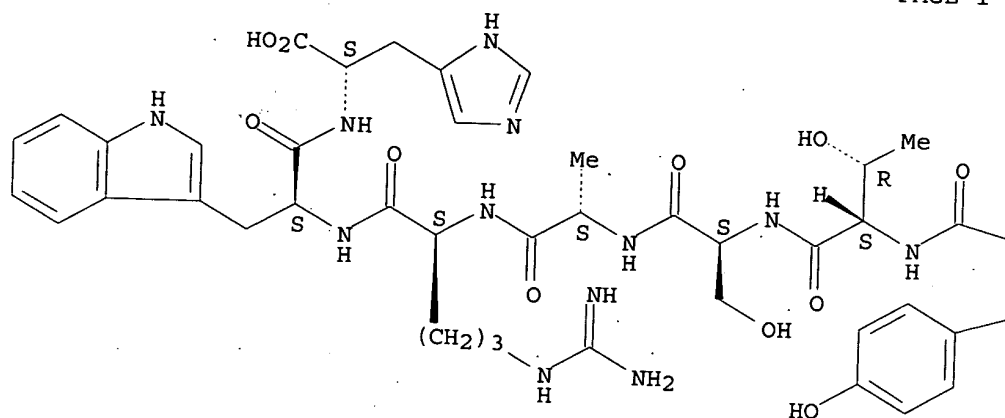
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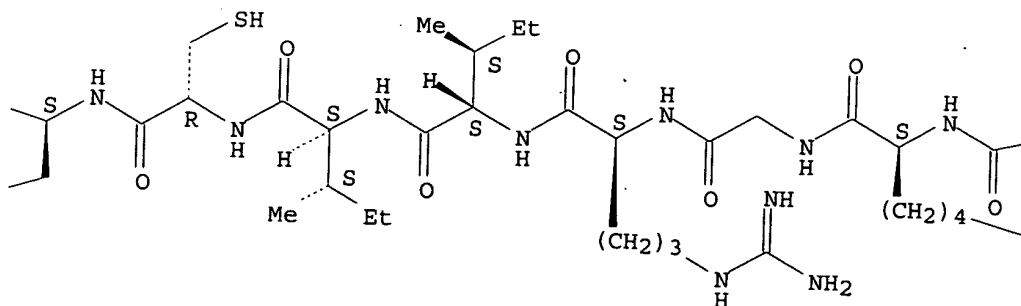
LC STN Files: CA, CAPLUS, USPATFULL

Absolute stereochemistry.

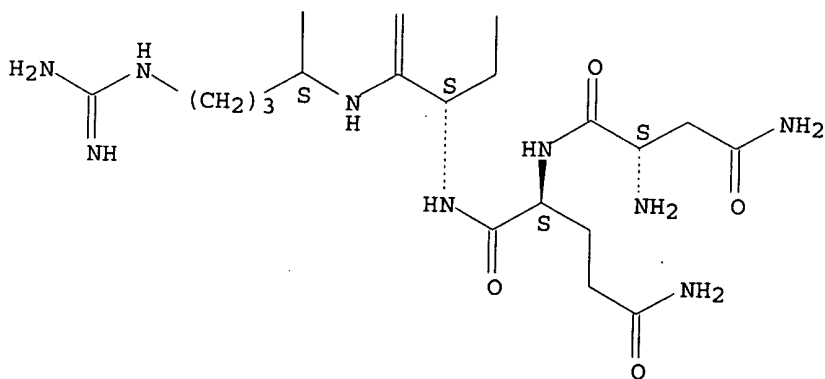
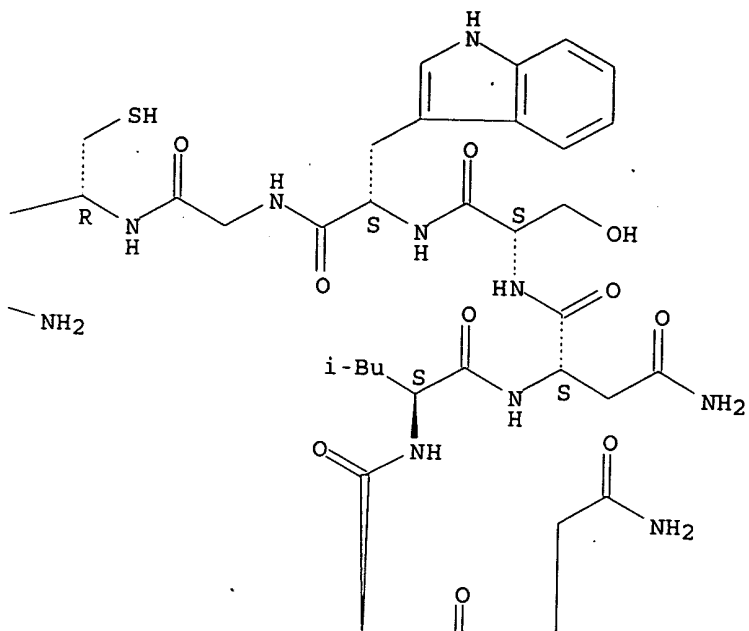
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PAGE 1-B



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1 REFERENCES IN FILE CA (1957 TO DATE)
1 REFERENCES IN FILE CAPLUS (1957 TO DATE)

=> fil hcaplus

FILE 'HCAPLUS' ENTERED AT 10:59:08 ON 05 JUN 2003

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FILE COVERS 1907 - 5 Jun 2003 VOL 138 ISS 23
FILE LAST UPDATED: 4 Jun 2003 (20030604/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

'OBI' IS DEFAULT SEARCH FIELD FOR 'HCAPLUS' FILE

=> d que nos 15

L1 16 SEA FILE=REGISTRY ABB=ON PLU=ON LNSWGCKGRIICYTS/SQSP
L4 9 SEA FILE=REGISTRY ABB=ON PLU=ON L1 AND SQL<31
L5 1 SEA FILE=HCAPLUS ABB=ON PLU=ON L4

=> d .ca 15

L5 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:392837 HCAPLUS
DOCUMENT NUMBER: 133:55969
TITLE: Peptide for detection of Group O HIV-1 and use for diagnosis
INVENTOR(S): Deleys, Robert; Chen, Jan
PATENT ASSIGNEE(S): Ortho-Clinical Diagnostics, Inc., USA
SOURCE: Jpn. Kokai Tokkyo Koho, 103 pp.
CODEN: JKXXAF
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 2000157268	A2	20000613	JP 1999-338385	19991129
US 6149910	A	20001121	US 1999-433428	19991104
EP 1013766	A2	20000628	EP 1999-309491	19991129
EP 1013766	A3	20030129		

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO

PRIORITY APPLN. INFO.:

US 1998-110292P P 19981130
US 1999-119138P P 19990208
US 1999-433428 A 19991104

AB Disclosed are the peptides derived from the immunodominant region of the Group O HIV-1 gp41 envelope protein, which do not correspond to any known naturally occurring Group O sequence or variant. The peptides bind to the antibodies to Group O HIV-1. The peptides are useful in detecting antibodies arise from the infection by Group O HIV-1. The peptides may be prepd. in a hybrid form with that of Group M HIV-1.

IC ICM C12N015-00
ICS C07K014-16; C07K016-12; C12N001-15; C12N001-19; C12N001-21; C12N005-10; C12P021-02; G01N033-569; C12P021-08

CC 10-1 (Microbial, Algal, and Fungal Biochemistry)

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Section cross-reference(s): 14
 IT 276687-00-4 276687-01-5 276694-91-8
 276873-37-1
 RL: ARG (Analytical reagent use); BSU (Biological study, unclassified);
 THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study);
 USES (Uses)
 (antibody to Group O HIV-1 detection by; peptide for detection of Group
 O HIV-1 and use for diagnosis)
 IT 275389-20-3 275389-22-5 275829-31-7 276250-39-6 276250-40-9
 276250-41-0 276250-42-1 276250-43-2 276250-47-6
 276250-48-7 276250-49-8 276250-50-1 276873-73-5
 RL: PRP (Properties)
 (unclaimed protein sequence; peptide for detection of Group O HIV-1 and
 use for diagnosis)
 IT 173145-89-6 275389-13-4 275389-14-5 275389-15-6 275389-16-7
 275389-17-8 275389-18-9 275389-19-0 275801-47-3
 275801-51-9 275801-52-0 275801-53-1 275829-37-3
 276249-52-6 276249-53-7 276249-62-8 276249-72-0 276249-78-6
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 276249-84-4 276249-86-6 276249-87-7 276249-88-8 276249-90-2
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 276249-97-9 276249-98-0 276249-99-1 276250-00-1 276250-01-2
 276250-02-3 276250-03-4 276250-04-5 276250-25-0 276250-26-1
 276250-27-2 276250-28-3 276250-29-4 276250-30-7 276250-31-8
 276250-32-9 276250-33-0 276250-34-1 276250-35-2 276250-36-3
 276250-37-4
 RL: PRP (Properties)
 (unclaimed sequence; peptide for detection of Group O HIV-1 and use for
 diagnosis)

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 5, 2003, 07:21:32 ; Search time 13 Seconds

(without alignments)
33.950 Million cell updates/sec

Title: US-09-605-573a-69_COPY_12_26

Perfect score: .89

Sequence: 1 LNSWGCKGRITCYTS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 segs, 29422922 residues

Total number of hits satisfying chosen parameters: 136623

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	72	80.9	15	1	US-08-615-279-8
2	72	80.9	15	1	US-08-615-279-8
3	68	76.4	19	1	US-08-472-597A-4
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5	63	70.8	19	1	US-08-472-597A-3
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7	59	66.3	19	1	US-08-472-597A-2
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9	56	62.9	14	4	US-08-682-791B-7
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11	55	61.8	14	4	US-08-682-791B-11
12	55	61.8	16	1	US-08-615-279-27
13	55	61.8	16	1	US-08-765-452-7
14	54	60.7	14	2	US-08-615-279-32
15	54	60.7	14	2	US-08-765-452-11
16	54	60.7	15	1	US-07-633-964-8
17	54	60.7	15	1	US-08-386-956-8
18	54	60.7	15	3	US-09-108-709-12
19	54	60.7	19	1	US-08-472-597A-1
20	54	60.7	19	1	US-08-837-732-1
21	53	59.6	12	2	US-08-146-028-5
22	53	59.6	12	4	US-08-723-425A-5
23	53	59.6	12	4	US-09-112-206-5
24	53	59.6	16	4	US-09-009-953-131
25	53	59.6	19	1	US-07-901-874B-14
26	53	59.6	19	1	US-08-457-865-14
27	53	59.6	20	1	US-07-633-964-14

28	53	59.6	20	1	US-08-386-956-14	Sequence 14, Appl
29	53	59.6	20	3	US-09-108-709-45	Sequence 45, Appl
30	53	59.6	21	2	US-08-146-028-2	Sequence 2, Appl1
31	53	59.6	21	4	US-08-723-425A-2	Sequence 2, Appl1
32	53	59.6	21	4	US-09-112-206-2	Sequence 2, Appl1
33	51	57.3	12	1	US-07-633-964-2	Sequence 2, Appl1
34	51	57.3	12	1	US-07-633-964-28	Sequence 28, Appl
35	51	57.3	12	1	US-07-633-964-29	Sequence 29, Appl
36	51	57.3	12	1	US-08-218-025A-121	Sequence 121, App
37	51	57.3	12	1	US-08-386-956-2	Sequence 2, Appl1
38	51	57.3	12	1	US-08-386-956-28	Sequence 28, Appl
39	51	57.3	12	1	US-08-386-956-29	Sequence 29, Appl
40	51	57.3	12	3	US-09-108-709-2	Sequence 2, Appl1
41	51	57.3	12	3	US-09-108-709-2	Sequence 2, Appl1
42	51	57.3	12	3	US-08-776-949-17	Sequence 17, Appl
43	51	57.3	13	3	US-08-108-709-18	Sequence 18, Appl
44	51	57.3	13	3	US-09-108-709-19	Sequence 19, Appl
45	51	57.3	13	3	US-09-108-709-20	Sequence 20, Appl
46	50	56.2	12	1	US-07-633-964-4	Sequence 4, Appl1
47	50	56.2	12	1	US-08-386-956-4	Sequence 4, Appl1
48	50	56.2	12	3	US-09-108-709-25	Sequence 25, Appl
49	50	56.2	13	3	US-09-108-709-26	Sequence 26, Appl
50	50	56.2	13	3	US-09-108-709-27	Sequence 27, Appl
51	50	56.2	14	3	US-09-108-709-28	Sequence 28, Appl
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55	50	56.2	18	6	5439792-3	Patent No. 5439792
56	50	56.2	20	6	5439792-8	Patent No. 5439792
57	50	56.2	9	3	US-09-108-709-23	Sequence 23, Appl
58	49	55.1	10	2	US-08-737-085A-10	Sequence 10, Appl
59	49	55.1	10	3	US-09-108-709-22	Sequence 22, Appl
60	49	55.1	10	3	US-09-246-258-10	Sequence 10, Appl
61	49	55.1	10	4	US-09-532-106-10	Sequence 10, Appl
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63	49	55.1	10	4	US-09-839-666-10	Sequence 10, Appl
64	49	55.1	11	3	US-09-108-709-21	Sequence 21, Appl
65	49	55.1	12	2	US-08-146-028-176	Sequence 176, App
66	49	55.1	12	2	US-08-146-028-177	Sequence 177, App
67	49	55.1	12	4	US-08-723-425A-176	Sequence 176, App
68	49	55.1	12	4	US-08-723-425A-177	Sequence 177, App
69	49	55.1	12	4	US-09-112-206-176	Sequence 176, App
70	49	55.1	12	4	US-09-112-206-177	Sequence 177, App
71	48	53.9	13	4	US-08-682-791B-1	Sequence 1, Appl1
72	48	53.9	14	4	US-08-682-791B-5	Sequence 5, Appl1
73	47	52.8	12	1	US-07-633-964-3	Sequence 3, Appl1
74	47	52.8	12	1	US-08-386-956-3	Sequence 3, Appl1
75	47	52.8	13	3	US-09-108-709-34	Sequence 34, Appl
76	47	52.8	13	3	US-09-108-709-35	Sequence 35, Appl
77	47	52.8	13	3	US-09-108-709-36	Sequence 36, Appl
78	47	52.8	14	3	US-09-108-709-37	Sequence 37, Appl
79	46	51.7	11	3	US-09-108-709-39	Sequence 39, Appl
80	46	51.7	14	4	US-08-682-791B-10	Sequence 10, Appl
81	45	50.6	12	2	US-08-146-028-24	Sequence 24, Appl
82	45	50.6	12	4	US-08-723-425A-24	Sequence 24, Appl
83	45	50.6	12	4	US-09-112-206-24	Sequence 24, Appl
84	44	49.4	12	3	US-08-776-949-29	Sequence 29, Appl
85	43	48.3	11	3	US-08-776-949-38	Sequence 38, Appl
86	43	48.3	13	3	US-08-776-949-38	Sequence 38, Appl
87	42	47.2	15	1	US-07-633-964-9	Sequence 9, Appl1
88	42	47.2	15	1	US-08-386-956-9	Sequence 9, Appl1
89	42	47.2	15	3	US-09-108-709-13	Sequence 13, Appl
90	42	47.2	17	1	US-07-633-964-5	Sequence 5, Appl1
91	42	47.2	17	1	US-08-386-956-5	Sequence 5, Appl1
92	42	47.2	17	2	US-08-833-556-1	Sequence 1, Appl1
93	42	47.2	17	3	US-09-108-709-6	Sequence 6, Appl1
94	42	47.2	17	4	US-09-388-664-1	Sequence 1, Appl1
95	42	47.2	19	2	US-08-765-452-8	Sequence 8, Appl1
96	41	46.1	10	1	US-07-633-964-21	Sequence 21, Appl
97	41	46.1	10	1	US-08-386-956-21	Sequence 21, Appl
98	41	46.1	10	3	US-09-108-709-16	Sequence 16, Appl
99	41	46.1	14	4	US-08-682-791B-6	Sequence 6, Appl1
100	41	46.1	14	4	US-08-682-791B-6	Sequence 6, Appl1

ALIGNMENTS

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RESULT 1
US-08-615-279-8
; Sequence 8, Application US/08615279
; Patent No. 5804371
;
; GENERAL INFORMATION:
; APPLICANT: H SS, Eva
; APPLICANT: SEIDEL, Christoph
; APPLICANT: WIENHUES, Ursula-Henrike
; APPLICANT: FAATZ, Elke
; APPLICANT: SCHMITT, Urban
; TITLE OF INVENTION: HAPTEN-LABELLED PEPTIDES
; NUMBER OF SEQUENCES: 40
;
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY & ORAM LLP
; STREET: 655 Fifteenth Street, N. W., Suite 330 - G
; STREET: Street Lobby
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/615,279
; FILING DATE: 25-MAR-1996
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 29:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/02921
; FILING DATE: 24-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BERMAN, Richard J.
; REGISTRATION NUMBER: 39,107
; REFERENCE/DOCKET NUMBER: P564-6006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
;
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Human immunodeficiency virus type 1
; STRAIN: subtype O
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 9p41
;
US-08-615-279-8
;
Query Match 80.9%; Score 72; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 7.9e-05;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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QY 1 LNSWCGKGRICVTS 15
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Db 1 LSLWCGKGRIVCVTS 15

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RESULT 2
US-08-615-279-29
; Sequence 29, Application US/08615279
; Patent No. 5804371
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; GENERAL INFORMATION:
; APPLICANT: H SS, Eva

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; APPLICANT: SEIDEL, Christoph
; APPLICANT: WIENHUES, Ursula-Henrike
; APPLICANT: FAATZ, Elke
; APPLICANT: SCHMITT, Urban
; TITLE OF INVENTION: HAPTEN-LABELLED PEPTIDES
; NUMBER OF SEQUENCES: 40
;
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY & ORAM LLP
; STREET: 655 Fifteenth Street, N. W., Suite 330 - G
; STREET: Street Lobby
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/615,279
; FILING DATE: 25-MAR-1996
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 29:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/02921
; FILING DATE: 24-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BERMAN, Richard J.
; REGISTRATION NUMBER: 39,107
; REFERENCE/DOCKET NUMBER: P564-6006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
;
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note=
; OTHER INFORMATION: "digoxigenin-3-cme-beta-alanine-epsilon-aminocaprolic
; OTHER INFORMATION: acid-beta-alanine is attached to the Leu at the 1 position
;
US-08-615-279-29
;
Query Match 80.9%; Score 72; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 7.9e-05;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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Db 1 LSLWCGKGRIVCVTS 15

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RESULT 3
US-08-472-597A-4
; Sequence 4, Application US/08472597A
; Patent No. 5624797
;
; GENERAL INFORMATION:
; APPLICANT: Bridon, D.P.
; APPLICANT: Size, I.S.Y.
; APPLICANT: Dagfal, D.J.
; APPLICANT: Jaffe, K.D.
; APPLICANT: Colpitts, T.L.
; TITLE OF INVENTION: Peptides for HIV-1 Detection
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: ABBOTT LABORATORIES
; STREET: ONE HUNDRED ABBOTT PARK ROAD
; CITY: ABBOTT PARK

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STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472.597A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-472-597A-4

Query Match 76.4%; Score 68; DB 1; Length 19;
Best Local Similarity 71.4%; Pred. No. 0.00039;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LNSWCGKGRILCYT 14
| |||||:
Db 6 LGIMGCKGKILCYT 19

RESULT 4
US-08-837-732-4
Sequence 4, Application US/08837732
Patent No. 5800983
GENERAL INFORMATION:
APPLICANT: Bridon, D.P.
APPLICANT: Size, I.S.Y.
APPLICANT: Dagbafal, D.J.
APPLICANT: Jaffe, K.D.
APPLICANT: Colpitts, T.L.
TITLE OF INVENTION: Peptides for HIV-1 Detection
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES
STREET: ONE HUNDRED ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837.732
FILING DATE: 23-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/472.597
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5765.US.01
TELECOMMUNICATION INFORMATION:

TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-837-732-4

Query Match 76.4%; Score 68; DB 1; Length 19;
Best Local Similarity 71.4%; Pred. No. 0.00039;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LNSWCGKGRILCYT 14
| |||||:
Db 6 LGIMGCKGKILCYT 19

RESULT 5
US-08-472-597A-3
Sequence 3, Application US/08472597A
Patent No. 5624797
GENERAL INFORMATION:
APPLICANT: Bridon, D.P.
APPLICANT: Size, I.S.Y.
APPLICANT: Dagbafal, D.J.
APPLICANT: Jaffe, K.D.
APPLICANT: Colpitts, T.L.
TITLE OF INVENTION: Peptides for HIV-1 Detection
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES
STREET: ONE HUNDRED ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472.597A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5765.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-472-597A-3

Query Match 70.8%; Score 63; DB 1; Length 19;
Best Local Similarity 64.3%; Pred. No. 0.0022;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LNSWCGKGRILCYT 14
| |||||:
Db 6 LGIMGCKGKILCYT 19

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RESULT 6
US-08-837-732-3
; Sequence 3, Application US/08837732
; Patent No. 5800983
; GENERAL INFORMATION:
; APPLICANT: Bridon, D.P.
; APPLICANT: Size, I.S.Y.
; APPLICANT: Dagfal, D.J.
; APPLICANT: Jaffe, K.D.
; APPLICANT: Colpits, T.L.
; TITLE OF INVENTION: Peptides for HIV-1 Detection
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES
; STREET: ONE HUNDRED ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,732
; FILING DATE: 22-Apr-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/472,597
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5765.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-837-732-3

Query Match          70.8%; Score 63; DB 1; Length 19;
Best Local Similarity 64.3%; Pred. No. 0.0022;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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RESULT 7
US-08-472-597A-2
; Sequence 2, Application US/08472597A
; Patent No. 5624797
; GENERAL INFORMATION:
; APPLICANT: Bridon, D.P.
; APPLICANT: Size, I.S.Y.
; APPLICANT: Dagfal, D.J.
; APPLICANT: Jaffe, K.D.
; APPLICANT: Colpits, T.L.
; TITLE OF INVENTION: Peptides for HIV-1 Detection
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES
; STREET: ONE HUNDRED ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL

QY 1 LNSWCKGRITCYT 14
DB 6 LGIWCCSGKLICTY 19

RESULT 8
US-08-837-732-2
; Sequence 2, Application US/08837732
; Patent No. 5800983
; GENERAL INFORMATION:
; APPLICANT: Bridon, D.P.
; APPLICANT: Size, I.S.Y.
; APPLICANT: Dagfal, D.J.
; APPLICANT: Jaffe, K.D.
; APPLICANT: Colpits, T.L.
; TITLE OF INVENTION: Peptides for HIV-1 Detection
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES
; STREET: ONE HUNDRED ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,732
; FILING DATE: 22-Apr-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/472,597
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5765.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365

QY 1 LNSWCKGRITCYT 14
DB 6 LGIWCCSGKLICTY 19

Query Match          66.3%; Score 59; DB 1; Length 19;
Best Local Similarity 64.3%; Pred. No. 0.0088;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-837-732-2

Query Match 66.3%; Score 59; DB 1; Length 19;
Best Local Similarity 64.3%; Pred. No. 0.0088;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 NSMCGKGRICCT 14
DB 6 LCMGCKGRICCT 19

RESULT 9

US-08-682-791B-7
Sequence 7, Application US/08682791B
Patent No. 6210901
GENERAL INFORMATION:
APPLICANT: SEIDEL, Christoph;
APPLICANT: HERMANN, Rupert;
APPLICANT: HOESS, Eva;
APPLICANT: BATZ Han-Georg
TITLE OF INVENTION: SPECIFIC BINDING SUBSTANCES FOR ANTIBODIES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,791B
FILING DATE: July 31, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6210901man D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: HUBR 1092
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 14
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
OTHER INFORMATION: Xaa 1s p-fluor-Phenylalanine
US-08-682-791B-7

Query Match 62.9%; Score 56; DB 4; Length 14;
Best Local Similarity 57.1%; Pred. No. 0.019;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NSMCGKGRICCT 15
DB 1 NSMCGAKRVCCHTT 14

RESULT 10

US-08-682-791B-8
Sequence 8, Application US/08682791B
Patent No. 6210901
GENERAL INFORMATION:
APPLICANT: SEIDEL, Christoph;
APPLICANT: HERMANN, Rupert;
APPLICANT: HOESS, Eva;
APPLICANT: BATZ Han-Georg
TITLE OF INVENTION: SPECIFIC BINDING SUBSTANCES FOR ANTIBODIES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,791B
FILING DATE: July 31, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6210901man D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: HUBR 1092
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 14
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
OTHER INFORMATION: Xaa 1s homo-Phenylalanine
US-08-682-791B-8

Query Match 62.9%; Score 56; DB 4; Length 14;
Best Local Similarity 57.1%; Pred. No. 0.019;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NSMCGKGRICCT 15
DB 1 NSMCGAKRVCCHTT 14

RESULT 11

US-08-682-791B-11
Sequence 11, Application US/08682791B
Patent No. 6210901
GENERAL INFORMATION:
APPLICANT: SEIDEL, Christoph;
APPLICANT: HERMANN, Rupert;
APPLICANT: HOESS, Eva;
APPLICANT: BATZ Han-Georg
TITLE OF INVENTION: SPECIFIC BINDING SUBSTANCES FOR ANTIBODIES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,791B
FILING DATE: July 31, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6210901man D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: HUBR 1092
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 688-3884
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 14
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
OTHER INFORMATION: Xaa is Nle
US-08-682-791B-11

Query Match 61.8%; Score 55; DB 4; Length 14;
Best Local Similarity 57.1%; Pred. No. 0.026;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 NSWGCKGRILCYTS 15
DB 1 NSWGCAFRXLCHTT 14

RESULT 12
US-08-615-279-27
Sequence 27, Application US/08615279
Patent No. 5804371
GENERAL INFORMATION:
APPLICANT: H SS, Eva
APPLICANT: SEIDEL, Christoph
APPLICANT: MIENHUES, Ursula-Henrike
APPLICANT: PAATZ, Elke
APPLICANT: SCHMITT, Urban
TITLE OF INVENTION: HAPTEN-LABELLED PEPTIDES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIIDO, MARMELESTEIN, MURRAY & ORAM LLP
STREET: 655 Fifteenth Street, N. W., Suite 330 - G
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,279
FILING DATE: 25-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/02921
FILING DATE: 24-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BERMAN, Richard J.
REGISTRATION NUMBER: 39,107
REFERENCE/DOCKET NUMBER: P564-6006
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000

TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note="cme-3-digoxigenin-1s
OTHER INFORMATION: "digoxigenin-3-cme-beta-alanine-epsilon-aminocaproic
OTHER INFORMATION: acid-beta-alanine is attached to the Leu at the 1 position
FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: /note="cme-3-digoxigenin-1s
OTHER INFORMATION: attached to the Leu at the 10 position."
US-08-615-279-27

Query Match 61.8%; Score 55; DB 1; Length 16;
Best Local Similarity 53.3%; Pred. No. 0.03;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 LNSWGCKGRILCYTS 15
DB 1 LGIWGCKGKILCTTA 15

RESULT 13
US-08-765-452-7
Sequence 7, Application US/08765452
Patent No. 5981286
GENERAL INFORMATION:
APPLICANT: HERRMANN, Rupert
APPLICANT: JOSEL, Hans-Peter
APPLICANT: PAPPERT, Gunter
APPLICANT: VOGTLE, Fritz
APPLICANT: FROMMERBERGER, Bruno
APPLICANT: ISSBERNER, Jorg
TITLE OF INVENTION: HYDROPHILIC METAL COMPLEXES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marnelestein, Murray & Oram LLP
STREET: 655 15th Street, N.W., Suite 330 - G St.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,452
FILING DATE: 16-JAN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: JAHNS, Kristina M.
REGISTRATION NUMBER: 41,092
REFERENCE/DOCKET NUMBER: 564-6014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-5000
TELEFAX: (202) 638-4810
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-765-452-7

Query Match 61.8%; Score 55; DB 2; Length 16;
Best Local Similarity 53.3%; Pred. No. 0.03;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 NSMCGKRIICYS 15
DB 1 LGIMCGSKLICHTA 15

RESULT 14

US-08-615-279-32

Sequence 32, Application US/08615279
Patent No. 5804371
GENERAL INFORMATION:
APPLICANT: H SS, Eva
APPLICANT: SEIDEL, Christoph
APPLICANT: WIENHUES, Ursula-Henrike
APPLICANT: RAATZ, Elke
APPLICANT: SCHMITT, Urban
TITLE OF INVENTION: HAPTEN-LABELLED PEPTIDES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIKO, MARIELSTEIN, MURRAY & ORAM LLP
STREET: 655 Fifteenth Street, N. W., Suite 330 - G
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,279
FILING DATE: 25-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/02921
FILING DATE: 24-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BERMAN, Richard J.
REGISTRATION NUMBER: 39,107
REFERENCE/DOCKET NUMBER: P564-6006
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note=
OTHER INFORMATION: 'diogx/egenln-3-cme-epsilon-aminoacaprolic acid is attached to
OTHER INFORMATION: asn at the 1 position."
US-08-615-279-32

Query Match 60.7%; Score 54; DB 1; Length 14;
Best Local Similarity 57.1%; Pred. No. 0.037;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NSMCGKRIICYS 15
DB 1 NSMCGAFROYCHTT 14

RESULT 15

US-08-765-452-11

Sequence 11, Application US/08765452
Patent No. 5981286
GENERAL INFORMATION:
APPLICANT: HERRMANN, Rupert
APPLICANT: JOSEL, Hans-Peter
APPLICANT: PAPPERT, Gunter
APPLICANT: VOSTER, Fritz
APPLICANT: FROMBERGER, Bruno
APPLICANT: ISSBERNER, Jorg
TITLE OF INVENTION: HYDROPHILIC METAL COMPLEXES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIKO, MARIELSTEIN, MURRAY & Oram LLP
STREET: 655 15th Street, N.W., Suite 330 - G St.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,452
FILING DATE: 16-JAN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: JAHNS, Kristina M.
REGISTRATION NUMBER: 41,092
REFERENCE/DOCKET NUMBER: 564-6014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-5000
TELEFAX: (202) 638-4810
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-765-452-11

Query Match 60.7%; Score 54; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 0.037;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NSMCGKRIICYS 15
DB 1 NSMCGAFROYCHTT 14

RESULT 16

US-07-633-964-8

Sequence 8, Application US/07633964
Patent No. 5459060
GENERAL INFORMATION:
APPLICANT: COLTOPIA MD, Joseph P
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES DIRECTED
TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS (HIV-1)
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles S. Coltopia, Esq.
STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
STATE: TX
COUNTRY: USA

```

1      ZIP: 75270-2197
2      COMPUTER READABLE FORM:
3      MEDIUM TYPE: floppy disk
4      COMPUTER: IBM PC compatible
5      OPERATING SYSTEM: PC-DOS/MS-DOS
6      SOFTWARE: PatentIn Release #1.0, Version #1.25
7      CURRENT APPLICATION DATA:
8      APPLICATION NUMBER: US/07/633,964
9      FILING DATE: 19901226
10     CLASSIFICATION: 424
11     PRIOR APPLICATION DATA:
12     APPLICATION NUMBER: US 396751
13     FILING DATE: 24-AUG-1989
14     ATTORNEY/AGENT INFORMATION:
15     NAME: Coltroia, Charles S
16     REGISTRATION NUMBER: 27189
17     REFERENCE/DOCKET NUMBER: CLON B-28796
18     TELECOMMUNICATION INFORMATION:
19     TELEPHONE: (214) 939-4500
20     TELEFAX: (214) 939-4600
21     INFORMATION FOR SEQ ID NO: 8:
22     SEQUENCE CHARACTERISTICS:
23     LENGTH: 15 amino acids
24     TYPE: AMINO ACID
25     TOPOLOGY: linear
26     MOLECULE TYPE: peptide
27     HYPOTHETICAL: NO
28     FRAGMENT TYPE: internal
29
30 US-07-633-964-8

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US-08-386-956-8
? ? ? ? ?
? FRAGMENT TYPE: Internal
? HYPOTHETICAL: NO
? MOLECULE TYPE: Peptide
? TOPOLOGY: linear
? TYPE: amino acid
? LENGTH: 15 amino acids
? SEQUENCE CHARACTERISTICS:
? INFORMATION FOR SEQ ID NO: 8:
? TELEFAX: (214) 939-4600
? TELEPHONE: (214) 939-4500
Oy      1 LNSWGCKGRICVT 14
        | ||| :||| |
Db      2 LGIWGCKGLICTT 15

```

COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472.597A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-472-597A-1

Query Match 60.7%; Score 54; DB 1; Length 19;
Best Local Similarity 57.1%; Pred. No. 0.049;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 LNSWGCKGRITCT 14
Db 6 LGTWGCKGLICTT 19

RESULT 20
US-08-837-732-1
Sequence 1, Application US/08837732
Patent No. 5800983
GENERAL INFORMATION:
APPLICANT: Bridon, D.P.
APPLICANT: Size, I.S.Y.
APPLICANT: Daghfal, D.J.
APPLICANT: Jaffe, K.D.
APPLICANT: Colpitts, T.L.
TITLE OF INVENTION: Peptides for HIV-1 Detection
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES
STREET: ONE HUNDRED ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837.732
FILING DATE: 22-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/472.597
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365

TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-837-732-1

Query Match 60.7%; Score 54; DB 1; Length 19;
Best Local Similarity 57.1%; Pred. No. 0.049;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 LNSWGCKGRITCT 14
Db 6 LGTWGCKGLICTT 19

RESULT 21
US-08-146-028-5
Sequence 5, Application US/08146028
Patent No. 5891640
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THE
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES
NUMBER OF SEQUENCES: 453
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146.028
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Ant170
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
FEATURE:
NAME/KEY: Modified-site
LOCATION: 12
US-08-146-028-5

Query Match 59.6%; Score 53; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 0.045;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 WCKGRIIC 12
Db 3 WCKGKRLVC 11

RESULT 22
US-08-723-425A-5
Sequence 5, Application US/08723425A
Patent No. 6165730
GENERAL INFORMATION:
APPLICANT: DELEYS, ROBERT
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF

TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...
NUMBER OF SEQUENCES: 433
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE, P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,425A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SAOOF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 1487-13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Ant70
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
FEATURE:
NAME/KEY: Modified-site
LOCATION: 12
US-08-723-425A-5

Query Match 59.6%; Score 53; DB 4; Length 12;
Best Local Similarity 66.7%; Pred. No. 0.045;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 WCCKGRITC 12
|||||:::|
DB 3 WCCKGRKIVC 11

RESULT 23
US-09-112-206-5
Sequence 5, Application US/09112206
Patent No. 6210903
GENERAL INFORMATION:
APPLICANT: PROCESS FOR THE DETERMINATION OF PEPTIDES
TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
NUMBER OF SEQUENCES: 453
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/112,206
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/146,028

FILING DATE:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Ant70
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
FEATURE:
NAME/KEY: Modified-site
LOCATION: 12
US-09-112-206-5

Query Match 59.6%; Score 53; DB 4; Length 12;
Best Local Similarity 66.7%; Pred. No. 0.045;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 WCCKGRITC 12
|||||:::|
DB 3 WCCKGRKIVC 11

RESULT 24
US-09-009-953-131
Sequence 131, Application US/09009953
Patent No. 6413517
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Identification of Broadly
Reactive DR Restricted Epitopes
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,953
FILING DATE: 21-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,713
FILING DATE: 23-JAN-1997
APPLICATION NUMBER: US 60/037,432
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauer
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-011520US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 131:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 131:

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Charles S. Cotropia, Esq.
;; STREET: 1201 Elm Street, Suite 4500
;; CITY: Dallas
;; STATE: TX
;; COUNTRY: USA
;; ZIP: 75270-2197
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/633,964
;; FILING DATE: 19901226
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 396751
;; FILING DATE: 24-AUG-1989
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Cotropia, Charles S
;; REGISTRATION NUMBER: 27189
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (214) 939-4500
;; TELEFAX: (214) 939-4600
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: circular
;; MOLECULE TYPE: peptide
;; HYPOTHEICAL: NO
;; FRAGMENT TYPE: Internal
;;
;; US-07-633-964-14
;;
Query Match 59.6%; Score 53; DB 1; Length 20;
Best Local Similarity 58.3%; Pred. No. 0.073;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
;;
QY 4 WCGKGRITCYTS 15
||| |::||| |:
DB 3 WCGSGKLICTTA 14
;;
RESULT 28
US-08-386-956-14
; Sequence 14, Application US/08386956
; Patent No. 5777074
; GENERAL INFORMATION:
; APPLICANT: Cotropia MD, Joseph P
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES DIRECTED
; TITLE OF INVENTION: AGAINST THE TRANSMEMBRANE GLYCOPROTEIN (gp41) OF HUMAN
; TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS (HIV-1)
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles S. Cotropia, Esq.
; STREET: 1201 Elm Street, Suite 4500
; CITY: Dallas
; STATE: TX
; COUNTRY: USA
; ZIP: 75270-2197
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/386,956
; FILING DATE: 10-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/633964

;; FILING DATE: 26-DEC-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Cotropia, Charles S
;; REGISTRATION NUMBER: 27189
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (214) 939-4500
;; TELEFAX: (214) 939-4600
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: amino acid
;; TOPOLOGY: circular
;; MOLECULE TYPE: peptide
;; HYPOTHEICAL: NO
;; FRAGMENT TYPE: Internal
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;; US-08-386-956-14
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Query Match 59.6%; Score 53; DB 1; Length 20;
Best Local Similarity 58.3%; Pred. No. 0.073;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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QY 4 WCGKGRITCYTS 15
||| |::||| |:
DB 3 WCGSGKLICTTA 14
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RESULT 29
US-09-108-709-45
; Sequence 45, Application US/09108709
; Patent No. 6008044
; GENERAL INFORMATION:
; APPLICANT: Cotropia, Joseph P.
; TITLE OF INVENTION: Human Monoclonal Antibodies Directed Against the Transmembrane
; TITLE OF INVENTION: Detecting the Presence and Concentration of Antibodies Inhibit
; TITLE OF INVENTION: Fusion-associated Epitope (GCSGRLIC) in gp-41
; FILE REFERENCE: 10586/00406
; CURRENT FILING DATE: 1998-07-01
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 45
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(20)
; OTHER INFORMATION: amino acids 599-618 according to Gann numbering
; OTHER INFORMATION: system
; US-09-108-709-45
;;
Query Match 59.6%; Score 53; DB 3; Length 20;
Best Local Similarity 58.3%; Pred. No. 0.073;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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QY 4 WCGKGRITCYTS 15
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DB 3 WCGSGKLICTTA 14
;;
RESULT 30
US-08-146-028-2
; Sequence 2, Application US/08146028
; Patent No. 5891640
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THE
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM

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: NUMBER OF SEQUENCES: 453
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/146,028
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 21 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: Peptide
: HYPOTHEICAL: NO
: ORIGINAL SOURCE:
: INDIVIDUAL ISOLATE: HIV-1
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 21
: US-08-146-028-2

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Query Match 59.6%; Score 53; DB 2; Length 21;
Best Local Similarity 58.3%; Pred. No. 0.076;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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DB 3 WCGSGKLCCTTA 14

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Search completed: June 5, 2003, 07:23:12
 Job time : 15 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 5, 2003, 07:21:57 ; Search time 228 Seconds
(without alignments)
6.792 Million cell updates/sec

Title: US-09-605-573a-69_COPY_12_26
Perfect score: 89
Sequence: 1 LNSWCKGRITCYTS 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters: 80475

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubppaa/PTCT_NEW_PUB pep.*
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- 10: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB pep.*
- 11: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB pep.*
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- 13: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB pep.*
- 14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	53	59.6	16	9	US-09-423-863-5
3	52	58.4	16	9	US-09-423-863-4
4	51	57.3	21	9	US-09-845-042-23
5	50	56.2	16	9	US-09-423-863-3
6	50	56.2	16	9	US-09-423-863-6
7	49	55.1	10	10	US-09-839-666-10
8	49	55.1	16	9	US-09-423-863-1
9	42	47.2	17	9	US-09-388-847-1
10	40	44.9	9	1	US-08-821-739A-78
11	40	44.9	9	10	US-09-894-018-80
12	40	44.9	9	10	US-09-894-018-185
13	37	41.6	10	10	US-09-765-086-43
14	36	40.4	6	9	US-10-026-741-41
15	36	40.4	10	1	US-08-821-739A-90
16	35	39.3	20	9	US-09-910-009A-481
17	34	38.2	7	9	US-10-026-741-5
18	34	38.2	10	9	US-09-423-863-10
19	34	38.2	10	9	US-09-423-863-11

20	33	37.1	10	9	US-09-423-863-9	Sequence 9, Appl
21	33	37.1	10	9	US-09-845-612B-14	Sequence 14, Appl
22	31	34.8	15	9	US-09-423-863-8	Sequence 8, Appl
23	31	34.8	13	9	US-09-910-009A-416	Sequence 416, Appl
24	31	34.8	18	9	US-10-142-238A-49	Sequence 49, Appl
25	30	33.7	10	9	US-09-423-863-7	Sequence 7, Appl
26	30	33.7	10	9	US-09-572-004B-922	Sequence 922, Appl
27	30	33.7	14	10	US-09-969-192-68	Sequence 68, Appl
28	30	33.7	21	9	US-09-974-879-281	Sequence 281, Appl
29	30	33.7	21	9	US-09-305-736-269	Sequence 269, Appl
30	29	32.6	14	9	US-09-999-724-93	Sequence 93, Appl
31	29	32.6	15	10	US-09-073-009-59	Sequence 59, Appl
32	29	32.6	15	10	US-09-023-588-59	Sequence 59, Appl
33	29	32.6	15	10	US-09-793-306-59	Sequence 31, Appl
34	29	32.6	15	10	US-09-969-192-31	Sequence 58, Appl
35	29	32.6	16	10	US-09-073-009-58	Sequence 58, Appl
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42	28	31.5	16	9	US-09-910-009A-247	Sequence 247, Appl
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51	27	30.3	13	10	US-09-784-887B-5	Sequence 5, Appl
52	27	30.3	13	9	US-10-087-714-4	Sequence 4, Appl
53	27	30.3	13	9	US-10-185-050-69	Sequence 6, Appl
54	27	30.3	14	9	US-10-029-301-5	Sequence 3, Appl
55	27	30.3	14	9	US-09-929-266-73	Sequence 3, Appl
56	27	30.3	15	9	US-09-932-613-74	Sequence 426, Appl
57	27	30.3	17	9	US-09-910-009A-426	Sequence 41378, A
58	27	30.3	17	10	US-09-864-761-41378	Sequence 427, Appl
59	27	30.3	18	9	US-09-910-009A-427	Sequence 245, Appl
60	27	30.3	19	10	US-10-092-750-245	Sequence 48329, A
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62	27	30.3	20	10	US-09-864-761-44019	Sequence 42, Appl
63	26	29.2	5	8	US-08-239-765B-4	Sequence 2155, Ap
64	26	29.2	5	9	US-09-042-888B-2	Sequence 297, App
65	26	29.2	5	9	US-09-949-278-2	Sequence 182, Appl
66	26	29.2	5	9	US-10-300-757-23	Sequence 38, Appl
67	26	29.2	5	10	US-09-815-156-2	Sequence 23, Appl
68	26	29.2	8	9	US-10-094-401-182	Sequence 2, Appl
69	26	29.2	9	9	US-09-835-948-38	Sequence 182, Appl
70	26	29.2	9	10	US-09-920-174-42	Sequence 42, Appl
71	26	29.2	10	9	US-09-572-404B-2155	Sequence 2113, Ap
72	26	29.2	11	10	US-09-780-070-26	Sequence 2155, Ap
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77	26	29.2	15	9	US-09-997-961-18	Sequence 18, Appl
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83	26	29.2	16	9	US-09-910-009A-408	Sequence 14, Appl
84	26	29.2	17	9	US-09-846-091-8	Sequence 408, App
85	26	29.2	17	9	US-10-012-756-16	Sequence 8, Appl
86	26	29.2	18	10	US-09-864-761-38674	Sequence 38674, A
87	26	29.2	18	10	US-09-747-029A-17	Sequence 16, Appl
88	26	29.2	19	10	US-09-864-761-37007	Sequence 37007, A
89	26	29.2	20	8	US-08-592-711-8	Sequence 37007, A
90	26	29.2	20	8	US-09-843-616-194	Sequence 194, App
91	26	29.2	20	9	US-09-973-025-75	Sequence 75, Appl
92	26	29.2	20	9	US-09-973-025-75	Sequence 75, Appl

93	26	29.2	20	9	US-09-438-486-194	Sequence 194, App
94	26	29.2	20	9	US-10-053-758-194	Sequence 194, App
95	26	29.2	20	9	US-09-899-303-75	Sequence 73, Appl
96	26	29.2	20	9	US-10-054-295-194	Sequence 194, App
97	26	29.2	20	9	US-10-083-357-1028	Sequence 1028, App
98	26	29.2	20	9	US-10-054-611-194	Sequence 194, App
99	26	29.2	20	9	US-10-023-282-902	Sequence 902, App
100	26	29.2	20	9	US-09-955-808-75	Sequence 75, Appl

ALIGNMENTS

RESULT 1
US-09-423-863-2
Sequence 2, Application US/09423863
Publication No. US20030054336A1
GENERAL INFORMATION:
APPLICANT: Donie, Frederic
APPLICANT: Faatz, Elke
APPLICANT: Hoess, Eva
TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND
FILE REFERENCE: BMID 9974 4638/OP/US-Sz
CURRENT APPLICATION NUMBER: US/09/423,863
CURRENT FILING DATE: 2000-02-08
EARLIER APPLICATION NUMBER: DE 19720914.9
EARLIER FILING DATE: 1997-05-16
EARLIER APPLICATION NUMBER: PCT/EP98/02816
EARLIER FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 16
TYPE: PRT
ORGANISM: Human Immunodeficiency virus type 1
US-09-423-863-2

Query Match 59.6%; Score 53; DB 9; Length 16;
Best Local Similarity 60.0%; Pred. No. 0.078;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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1 LIGWCGSGRHICTT 15

RESULT 2
US-09-423-863-5
Sequence 5, Application US/09423863
Publication No. US20030054336A1
GENERAL INFORMATION:
APPLICANT: Donie, Frederic
APPLICANT: Faatz, Elke
APPLICANT: Hoess, Eva
TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND
FILE REFERENCE: BMID 9974 4638/OP/US-Sz
CURRENT APPLICATION NUMBER: US/09/423,863
CURRENT FILING DATE: 2000-02-08
EARLIER APPLICATION NUMBER: DE 19720914.9
EARLIER FILING DATE: 1997-05-16
EARLIER APPLICATION NUMBER: PCT/EP98/02816
EARLIER FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 16
TYPE: PRT
ORGANISM: Human Immunodeficiency virus type 1
US-09-423-863-5

Query Match 59.6%; Score 53; DB 9; Length 16;

Best Local Similarity 60.0%; Pred. No. 0.078;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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1 LIGWCGSGRHICTT 15

RESULT 3
US-09-423-863-4
Sequence 4, Application US/09423863
Publication No. US20030054336A1
GENERAL INFORMATION:
APPLICANT: Donie, Frederic
APPLICANT: Faatz, Elke
APPLICANT: Hoess, Eva
TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND
FILE REFERENCE: BMID 9974 4638/OP/US-Sz
CURRENT APPLICATION NUMBER: US/09/423,863
CURRENT FILING DATE: 2000-02-08
EARLIER APPLICATION NUMBER: DE 19720914.9
EARLIER FILING DATE: 1997-05-16
EARLIER APPLICATION NUMBER: PCT/EP98/02816
EARLIER FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 16
TYPE: PRT
ORGANISM: Human Immunodeficiency virus type 1
US-09-423-863-4

Query Match 58.4%; Score 52; DB 9; Length 16;
Best Local Similarity 64.3%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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1 LIGWCGSGRHICTT 14

RESULT 4
US-09-845-042-23
Sequence 23, Application US/09845042
Publication No. US20030092177A1
GENERAL INFORMATION:
APPLICANT: BELARDELLI, FILIPPO
APPLICANT: SANTINI, STEFANO MARIA
APPLICANT: PARLATO, STEFANIA
APPLICANT: DI PUCCHIO, TIZIANA
APPLICANT: LOGOZZI, MARIANTONIA
APPLICANT: LAPENTA, CATERINA
APPLICANT: FERRANTINI, MARIA
APPLICANT: SANTODONATO, LORA
APPLICANT: D'AGOSTINO, GIUSEPPINA
TITLE OF INVENTION: METHOD FOR GENERATING HIGHLY ACTIVE HUMAN DENDRITIC
FILE REFERENCE: 618742-8/JP/B-4161
CURRENT APPLICATION NUMBER: US/09/845,042
CURRENT FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 21
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus type 1
US-09-845-042-23

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Best Local Similarity 58.3%; Pred. No. 0.2;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 LNSGCKGRITC 12
 Db 10 LGIMCSCGKILIC 21

RESULT 5
 US-09-423-863-3

; Sequence 3, Application US/09423863
 ; Publication No. US20030054336A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Donle, Frederic
 ; APPLICANT: Faatz, Elke
 ; APPLICANT: Hoess, Eva
 ; TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND
 ; FILE REFERENCE: BMID 9974 4638/OP/US-S2
 ; CURRENT APPLICATION NUMBER: US/09/423,863
 ; CURRENT FILING DATE: 2000-02-08
 ; EARLIER APPLICATION NUMBER: DE 19720914.9
 ; EARLIER FILING DATE: 1997-05-16
 ; EARLIER APPLICATION NUMBER: PCT/EP98/02816
 ; EARLIER FILING DATE: 1998-05-13
 ; NUMBER OF SEQ ID NOS: 12
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 ; SEQ ID NO: 3
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Human Immunodeficiency virus type 1
 US-09-423-863-3

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 Best Local Similarity 53.3%; Pred. No. 0.23;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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 Db 1 LGIMCSCGKHCITN 15

RESULT 6
 US-09-423-863-6

; Sequence 6, Application US/09423863
 ; Publication No. US20030054336A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Donle, Frederic
 ; APPLICANT: Faatz, Elke
 ; APPLICANT: Hoess, Eva
 ; TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND
 ; FILE REFERENCE: BMID 9974 4638/OP/US-S2
 ; CURRENT APPLICATION NUMBER: US/09/423,863
 ; CURRENT FILING DATE: 2000-02-08
 ; EARLIER APPLICATION NUMBER: DE 19720914.9
 ; EARLIER FILING DATE: 1997-05-16
 ; EARLIER APPLICATION NUMBER: PCT/EP98/02816
 ; EARLIER FILING DATE: 1998-05-13
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 6
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Human Immunodeficiency virus type 1
 US-09-423-863-6

Query Match 56.2%; Score 50; DB 9; Length 16;
 Best Local Similarity 53.3%; Pred. No. 0.23;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 LNSGCKGRITCYTS 15
 Db 1 LGIMCSCGKHCITN 15

RESULT 7
 US-09-839-666-10

; Sequence 10, Application US/09839666
 ; Patent No. US20020025513A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SALBERG, MATTI
 ; TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
 ; EXCHANGER
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DARBY & DARBY PC
 ; STREET: 805 Third Avenue
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10022
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; OPERATING SYSTEM: IBM Compatible
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/839,666
 ; FILING DATE: 19-Apr-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/737,085
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Green, Reza
 ; REGISTRATION NUMBER: 38,475
 ; REFERENCE/DOCKET NUMBER: 3846/0C569
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-527-7659
 ; TELEFAX: 212-753-6237
 ; TELEX: 236687
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-839-666-10

Query Match 55.1%; Score 49; DB 10; Length 10;
 Best Local Similarity 66.7%; Pred. No. 0.21;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 WCGCKGRITC 12
 Db 1 WCGSKLIC 9

RESULT 8
 US-09-423-863-1

; Sequence 1, Application US/09423863
 ; Publication No. US20030054336A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Donle, Frederic
 ; APPLICANT: Faatz, Elke
 ; APPLICANT: Hoess, Eva
 ; TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND
 ; FILE REFERENCE: BMID 9974 4638/OP/US-S2
 ; CURRENT APPLICATION NUMBER: US/09/423,863
 ; CURRENT FILING DATE: 2000-02-08
 ; EARLIER APPLICATION NUMBER: DE 19720914.9
 ; EARLIER FILING DATE: 1997-05-16
 ; EARLIER APPLICATION NUMBER: PCT/EP98/02816
 ; EARLIER FILING DATE: 1998-05-13
 ; NUMBER OF SEQ ID NOS: 12

1

FEATURE:
OTHER INFORMATION: Oligopeptide
US-09-894-018-80

Query Match
Best Local Similarity 44.9%; Score 40; DB 10; Length 9;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 WCCGRII 11
DB 2 WCCSGKLI 9

RESULT 12
US-09-894-018-185
Sequence 185, Application US/09894018
Patent No. US20020119127A1
GENERAL INFORMATION:
APPLICANT: EPIMUNE, Inc.
APPLICANT: Sette, Alessandro
APPLICANT: Chestnut, Robert
APPLICANT: Livingston, Brian
APPLICANT: Baker, Dennis
APPLICANT: Newman, Mark
TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
FILE REFERENCE: 39963-2003.00
CURRENT APPLICATION NUMBER: US/09/894,018
PRIOR FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: PCT/US00/35568
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/173,390
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: US 60/284,221
NUMBER OF SEQ ID NOS: 368
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 185
LENGTH: 9
TYPE: PRT
ORGANISM: Transgenic mouse
US-09-894-018-185

Query Match
Best Local Similarity 44.9%; Score 40; DB 10; Length 9;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 WCCGRII 11
DB 2 WCCSGKLI 9

RESULT 13
US-09-765-086-43
Sequence 43, Application US/09765086
Patent No. US20010046498A1
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Pasqualini, Renata
APPLICANT: Madh, Arap
APPLICANT: Bredesen, Dale E.
APPLICANT: Ellerby, H. Michael
TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With
FILE REFERENCE: P-LJ 3844
CURRENT APPLICATION NUMBER: US/09/765,086
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US 09/489,582
NUMBER OF SEQ ID NOS: 235
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 43

LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
US-09-765-086-43

Query Match
Best Local Similarity 41.6%; Score 37; DB 10; Length 10;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 WCCGR 9
DB 2 WCCNGR 7

RESULT 14
US-10-026-741-41
Sequence 41, Application US/10026741
Publication No. US20030049604A1
GENERAL INFORMATION:
APPLICANT: CHARNEAU, PIERRE
CLAVEL, FRANCOISE
BORMAN, ANDREW
QUILLIENT, CAROLINE
GUETARD, DENISE
MONTAGNIER, LUC
DONON DE SAINT-MARTIN, JACQUELINE
COHEN, JAOUES
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
SUBTYPE) ANTIGENS
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSER: Finnegan, Henderson, Farabow, Garrett &
Dunnet, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/026,741
FILING DATE: 27-Dec-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/817,441
FILING DATE: 31-AUG-1998
APPLICATION NUMBER: PCT/FR 95/01391
FILING DATE: 20-OCT-1995
APPLICATION NUMBER: FR 9412554
FILING DATE: 20-OCT-1994
APPLICATION NUMBER: FR 9502526
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03660, 6005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-026-741-41

Query Match 40.4%; Score 36; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 3.3e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 WCKGR 9
11111
DB 1 WCKNR 6

RESULT 15

US-08-821-739A-90
; Sequence 90, Application US/08821739A
; Patent No. US20020168374A1
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 2060.005000A
; CURRENT APPLICATION NUMBER: US/08/821,739A
; CURRENT FILING DATE: 1999-03-20
; PRIOR APPLICATION NUMBER: 60/013,833
; PRIOR FILING DATE: 1996-03-21
; PRIOR APPLICATION NUMBER: 08/589,107
; PRIOR FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: 08/451,913
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: 07/926,666
; PRIOR FILING DATE: 1992-08-07
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-821-739A-90

Query Match 40.4%; Score 36; DB 1; Length 10;
Best Local Similarity 55.6%; Pred. No. 21;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LNSWGCKR 9
11111
DB 2 LGIWGCGK 10

RESULT 16
US-09-910-009A-481
; Sequence 481, Application US/09910009A
; Publication No. US20030050234A1
; GENERAL INFORMATION:

; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Oliveira, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.

; APPLICANT: Cartier, G. Edward
; APPLICANT: Shen, Greg S.
; APPLICANT: Magstaff, John D.
; TITLE OF INVENTION: Mu-Conopeptides
; FILE REFERENCE: 2314-242
; CURRENT APPLICATION NUMBER: US/09/910,009A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,619
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/245,157
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/264,319
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: US 60/277,270
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 520
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 481
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Conus ermineus
US-09-910-009A-481

Query Match 39.3%; Score 35; DB 9; Length 20;
Best Local Similarity 33.3%; Pred. No. 57;
Matches 5; Conservative 4; Mismatches 2; Indels 4; Gaps 1;

QY 3 SWGC---KGRITCY 13
11111
DB 3 SWPCRRISNGKIVCF 17

RESULT 17

US-10-026-741-5
; Sequence 5, Application US/10026741
; Publication No. US20030049604A1
; GENERAL INFORMATION:

; APPLICANT: CHARNEAU, PIERRE
; CLAVEL, FRANCOISE
; BORMAN, ANDREM
; OUILLENT, CAROLINE
; GUETARD, DENISE
; MONTAGNIER, LUC
; DONDON DE SAINT-MARTIN, JACQUELINE
; COHEN, JACQUES
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
SUBTYPE) ANTIGENS
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Flinnegan, Henderson, Farabow, Garrett &
; Dunner, L.L.P.
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/026,741
; FILING DATE: 27-Dec-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/817,441
; FILING DATE: 31-AUG-1998
; APPLICATION NUMBER: PCT/FR 95/01391
; FILING DATE: 20-OCT-1995
; APPLICATION NUMBER: FR 9412554
; FILING DATE: 20-OCT-1994
; APPLICATION NUMBER: FR 9502526
; FILING DATE: 03-MAR-1995

```
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03260, 6005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4000
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-026-741-5

Query Match      38.2% Score 34; DB 9; Length 7;
Best Local Similarity 71.4%; Pred. No. 3.5e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      6 CKGRICYS 12
      1 1 1 1 1
      1 CKNRLLC 7

Db

RESULT 18
US-09-423-863-10
; Sequence 10, Application US/09423863
; Publication No. US20030054336a1
; GENERAL INFORMATION:
; APPLICANT: Donle, Frederic
; APPLICANT: Faatz, Elke
; APPLICANT: Hoess, Eva
; TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND
; TITLE OF INVENTION: ANTIGENS USED IN IT
; FILE REFERENCE: BMID 9974 4638/OP/US-S2
; CURRENT APPLICATION NUMBER: US/09/423,863
; CURRENT FILING DATE: 2000-02-08
; EARLIER APPLICATION NUMBER: DE 19720914.9
; EARLIER FILING DATE: 1997-05-16
; EARLIER APPLICATION NUMBER: PCT/EP98/02816
; EARLIER FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-423-863-10

Query Match      38.2% Score 34; DB 9; Length 10;
Best Local Similarity 60.0%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      6 CKGRICYS 15
      1 1 1 1 1 1
      1 CSGRHICCTN 10

Db

RESULT 19
US-09-423-863-11
; Sequence 11, Application US/09423863
; Publication No. US20030054336a1
; GENERAL INFORMATION:
; APPLICANT: Donle, Frederic
; APPLICANT: Faatz, Elke
; APPLICANT: Hoess, Eva
; TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND
; TITLE OF INVENTION: ANTIGENS USED IN IT
; FILE REFERENCE: BMID 9974 4638/OP/US-S2
; CURRENT APPLICATION NUMBER: US/09/423,863
; CURRENT FILING DATE: 2000-02-08
```

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; EARLIER APPLICATION NUMBER: DE 19720914.9
; EARLIER FILING DATE: 1997-05-16
; EARLIER APPLICATION NUMBER: PCT/EP98/02816
; EARLIER FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-423-863-11

Query Match      38.2% Score 34; DB 9; Length 10;
Best Local Similarity 60.0%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      6 CKGRICYS 15
      1 1 1 1 1 1
      1 CSGRHICCTT 10

Db

RESULT 20
US-09-423-863-9
; Sequence 9, Application US/09423863
; Publication No. US20030054336a1
; GENERAL INFORMATION:
; APPLICANT: Donle, Frederic
; APPLICANT: Faatz, Elke
; APPLICANT: Hoess, Eva
; TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND
; TITLE OF INVENTION: ANTIGENS USED IN IT
; FILE REFERENCE: BMID 9974 4638/OP/US-S2
; CURRENT APPLICATION NUMBER: US/09/423,863
; CURRENT FILING DATE: 2000-02-08
; EARLIER APPLICATION NUMBER: DE 19720914.9
; EARLIER FILING DATE: 1997-05-16
; EARLIER APPLICATION NUMBER: PCT/EP98/02816
; EARLIER FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-423-863-9

Query Match      37.1% Score 33; DB 9; Length 10;
Best Local Similarity 66.7%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      6 CKGRICYS 14
      1 1 1 1 1
      1 CSGRHICCT 9

Db

RESULT 21
US-09-845-612B-14
; Sequence 14, Application US/09845612B
; Publication No. US20030083261a1
; GENERAL INFORMATION:
; APPLICANT: YU, HONGTAO
; APPLICANT: TANG, ZHANYUN
; APPLICANT: LUO, XUELIAN
; APPLICANT: RIZO-REY, JOSE
; TITLE OF INVENTION: A CLASS OF 12MER PEPTIDES THAT INHIBIT THE FUNCTION OF THE MIT
; FILE REFERENCE: UTSD:795
; CURRENT APPLICATION NUMBER: US/09/845,612B
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 15
```

TYPE: PRT
ORGANISM: Drosophila
US-09-845-612B-14

Query Match
Best Local Similarity 37.1%; Score 33; DB 9; Length 15;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 GRICCY 13
|:|:|:
DB 5 GRICCY 10

RESULT 22
US-09-423-863-8
Sequence 8, Application US/09423863
Publication No. US20030054336A1
GENERAL INFORMATION:

APPLICANT: Donle, Frederic
APPLICANT: Faatz, Elke
APPLICANT: Hoess, Eva
TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND

FILE REFERENCE: BMID 9974 4638/OP/US-S2
CURRENT APPLICATION NUMBER: US/09/423,863
CURRENT FILING DATE: 2000-02-08
EARLIER FILING DATE: 1997-05-16
EARLIER APPLICATION NUMBER: DE 19720914.9
EARLIER FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 8
LENGTH: 10
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-423-863-8

Query Match
Best Local Similarity 34.8%; Score 31; DB 9; Length 10;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 CCKRITCYTS 15
|:|:|:|:
DB 1 CCKGHICITTN 10

RESULT 23
US-09-910-009A-416
Sequence 416, Application US/09910009A
Publication No. US20030050234A1
GENERAL INFORMATION:

APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.

APPLICANT: McIntosh, J. Michael
APPLICANT: Garrett, James E.
APPLICANT: Watkins, Maren
APPLICANT: Cruz, Lourdes J.
APPLICANT: Shou, Ki-Joon
APPLICANT: Jacobsen, Richard
APPLICANT: Jones, Robert M.
APPLICANT: Cartier, G. Edward
APPLICANT: Shen, Greg S.
APPLICANT: Magstaff, John D.
TITLE OF INVENTION: Mu-Conopeptides
FILE REFERENCE: 2314-242

CURRENT APPLICATION NUMBER: US/09/910,009A
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/219,619
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/245,157
PRIOR FILING DATE: 2000-11-03

PRIOR APPLICATION NUMBER: US 60/264,319
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: US 60/277,270
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 520
SOFTWARE: PatentIn version 3.0
SEQ ID NO 416
LENGTH: 13
TYPE: PRT
ORGANISM: Conus laterculatus
US-09-910-009A-416

QY 4 WCKGRITC 12
|:|:|:|:
DB 4 WPCSGCIPC 12

Query Match
Best Local Similarity 34.8%; Score 31; DB 9; Length 13;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 WCKGRITC 12
|:|:|:|:
DB 4 WPCSGCIPC 12

RESULT 24
US-10-142-238A-49
Sequence 49, Application US/10142238A
Publication No. US20030087819A1
GENERAL INFORMATION:

APPLICANT: Bielschki, John K.
TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
FILE REFERENCE: IB-1705
CURRENT APPLICATION NUMBER: US/10/142,238A
CURRENT FILING DATE: 2002-08-19

PRIOR APPLICATION NUMBER: US 60/289,944
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PatentIn version 3.1
SEQ ID NO 49
LENGTH: 18
TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)-(18)
OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-49

QY 6 CCKRITCYTS 13
|:|:|:|:
DB 7 CCKRLVQY 14

Query Match
Best Local Similarity 34.8%; Score 31; DB 9; Length 18;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCKRITCYTS 13
|:|:|:|:
DB 7 CCKRLVQY 14

RESULT 25
US-09-423-863-7
Sequence 7, Application US/09423863
Publication No. US20030054336A1
GENERAL INFORMATION:

APPLICANT: Donle, Frederic
APPLICANT: Faatz, Elke
APPLICANT: Hoess, Eva
TITLE OF INVENTION: PROCESS FOR THE DETECTION OF HIV ANTIBODIES AND

FILE REFERENCE: BMID 9974 4638/OP/US-S2
CURRENT APPLICATION NUMBER: US/09/423,863
CURRENT FILING DATE: 2000-02-08
EARLIER FILING DATE: 1997-05-16
EARLIER APPLICATION NUMBER: DE 19720914.9
EARLIER FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 7
LENGTH: 10
TYPE: PRT
ORGANISM: Human Immunodeficiency virus type 1
US-09-423-863-7

Query Match 33.7% Score 30; DB 9; Length 10;
Best Local Similarity 55.6% Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Y 6 CKGRILCYT 14
| | | | |
Db 1 CCGKHICTT 9

RESULT 26
US-09-572-404B-922
Sequence 922, Application US/09572404B
Publication No. US20030078374A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProPatent version 1.0
SEQ ID NO 922
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
OTHER INFORMATION: sequence located in MPPA at 11-20 and may interact with sequence
US-09-572-404B-922

Query Match 33.7% Score 30; DB 9; Length 10;
Best Local Similarity 100.0% Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 3 SWGC 6
| | | |
Db 7 SWGC 10

RESULT 27
US-09-969-192-68

Sequence 68, Application US/09969192
Patent No. US20020151027A1
GENERAL INFORMATION:
APPLICANT: WICKHAM, THOMAS J.
ROELVINK, PETRUS W.
KOVESDI, IMRE

TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
CONSTRAINED PEPTIDE MOTIFS
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/969,192
FILING DATE: 01-Oct-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 9-455061

FILING DATE: 06-DEC-1999
APPLICATION NUMBER: US 9-130225
FILING DATE: 06-AUG-1998
APPLICATION NUMBER: US 8-701124
FILING DATE: 21-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Helner, M. Daniel
REGISTRATION NUMBER: 41,826
REFERENCE/DOCKET NUMBER: 213564
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-09-969-192-68

Query Match 33.7% Score 30; DB 10; Length 14;
Best Local Similarity 50.0% Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Y 6 CKGRICVTS 15
| | | | |
Db 5 CRGDCFCCT 14

RESULT 28
US-09-974-879-281
Sequence 281, Application US/09974879
Publication No. US20030028003A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 125 Human Secreted Proteins
FILE REFERENCE: P2020P2
CURRENT APPLICATION NUMBER: US/09/974,879
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/239,893
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 09/818,683
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 09/305,736
PRIOR FILING DATE: 1999-05-05
PRIOR APPLICATION NUMBER: PCT/US98/23435
PRIOR FILING DATE: 1998-11-04
PRIOR APPLICATION NUMBER: US 60/064,911
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064,912
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064,983
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064,900
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064,988
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064,987
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064,908
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064,984
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064,985
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/066,094
PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: US 60/066,100
PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: US 60/066,089
PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: US 60/066,095
PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: US 60/066,090

PRIOR FILING DATE: 1997-11-17
 NUMBER OF SEQ ID NOS: 611
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 281
 LENGTH: 21
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-974-879-281

Query Match 33.7%: Score 30; DB 9; Length 21;
 Best Local Similarity 71.4%: Pred. No. 3.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LNSWGCK 7
 1 1 1 1 1
 DB 10 LRSWGAK 16

RESULT 29
 US-09-305-736-269
 Sequence 269, Application US/09305736
 Publication No. US20030086078A1
 GENERAL INFORMATION:
 APPLICANT: Feng et al.
 TITLE OF INVENTION: 125 Human Secreted Proteins
 FILE REFERENCE: P2020P1
 CURRENT APPLICATION NUMBER: US/09/305,736
 CURRENT FILING DATE: 1999-05-05
 EARLIER APPLICATION NUMBER: PCT/US98/23435
 EARLIER FILING DATE: 1998-11-04
 EARLIER APPLICATION NUMBER: 60/064,911
 EARLIER FILING DATE: 1997-11-07
 EARLIER APPLICATION NUMBER: 60/064,912
 EARLIER FILING DATE: 1997-11-07
 EARLIER APPLICATION NUMBER: 60/064,983
 EARLIER FILING DATE: 1997-11-07
 EARLIER APPLICATION NUMBER: 60/064,900
 EARLIER FILING DATE: 1997-11-07
 EARLIER APPLICATION NUMBER: 60/064,988
 EARLIER FILING DATE: 1997-11-07
 EARLIER APPLICATION NUMBER: 60/064,987
 EARLIER FILING DATE: 1997-11-07
 EARLIER APPLICATION NUMBER: 60/064,908
 EARLIER FILING DATE: 1997-11-07
 EARLIER APPLICATION NUMBER: 60/064,984
 EARLIER FILING DATE: 1997-11-07
 EARLIER APPLICATION NUMBER: 60/064,985
 EARLIER FILING DATE: 1997-11-07
 EARLIER APPLICATION NUMBER: 60/066,094
 EARLIER FILING DATE: 1997-11-17
 EARLIER APPLICATION NUMBER: 60/066,100
 EARLIER FILING DATE: 1997-11-17
 EARLIER APPLICATION NUMBER: 60/066,089
 EARLIER FILING DATE: 1997-11-17
 EARLIER APPLICATION NUMBER: 60,066,095
 EARLIER FILING DATE: 1997-11-17
 EARLIER APPLICATION NUMBER: 60/066,090
 EARLIER FILING DATE: 1997-11-17
 NUMBER OF SEQ ID NOS: 612
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 269
 LENGTH: 21
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-305-736-269

Query Match 33.7%: Score 30; DB 9; Length 21;
 Best Local Similarity 71.4%: Pred. No. 3.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LNSWGCK 7
 1 1 1 1 1
 DB 10 LRSWGAK 16

RESULT 30
 US-09-999-724-93
 Sequence 93, Application US/09999724
 Publication No. US20030022355A1
 GENERAL INFORMATION:
 APPLICANT: WICKHAM, THOMAS J.
 APPLICANT: KOVESDI, IMRE
 APPLICANT: BROUGH, DOUGLAS E.
 TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER
 FILE REFERENCE: 212960
 CURRENT APPLICATION NUMBER: US/09/999,724
 CURRENT FILING DATE: 2001-10-24
 PRIOR APPLICATION NUMBER: US 09/101,751
 PRIOR FILING DATE: 1999-01-29
 PRIOR APPLICATION NUMBER: WO 96US19150
 PRIOR FILING DATE: 1996-11-27
 PRIOR APPLICATION NUMBER: US 08/700,846
 PRIOR FILING DATE: 1996-08-21
 PRIOR APPLICATION NUMBER: US 08/701,124
 PRIOR FILING DATE: 1996-08-21
 PRIOR APPLICATION NUMBER: US 08/563,368
 PRIOR FILING DATE: 1995-11-28
 NUMBER OF SEQ ID NOS: 94
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 93
 LENGTH: 14
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic
 US-09-999-724-93

Query Match 32.6%: Score 29; DB 9; Length 14;
 Best Local Similarity 50.0%: Pred. No. 3.5e+02;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 6 CKGRILCYTS 15
 1 1 1 1 1
 DB 5 CRGDFCGTS 14

Search completed: June 5, 2003, 07:27:41
 Job time: 230 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 08:58:43 ; Search time 15 Seconds

(without alignments)
96.134 Million cell updates/sec

Title: US-09-605-573A-69_COPY_12_26

Perfect score: 89

Sequence: 1 LNSMGCKGRICYS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: PIR_73:**
2: PIR1:**
3: PIR2:**
4: PIR3:**
5: PIR4:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	30.3	13	2	S57567 T cell receptor V-
2	27	30.3	20	2	S29635 jaccalin beta chain
3	26.5	29.8	15	2	S10386 Ig heavy chain J r
4	26	29.2	16	2	PC4416 ErbB kinase activa
5	26	29.2	19	1	EMSGAN ancoventin - strept
6	25.5	28.7	17	2	S24570 Ig heavy chain J r
7	25.5	28.7	19	2	A58700 actagardine (valid
8	25	28.1	14	2	PH1306 Ig heavy chain DJ
9	25	28.1	15	2	S02381 probable membrane
10	24.5	27.5	14	2	S03530 Ig heavy chain J r
11	24	27.0	10	2	A59173 nuclease Bhl (EC 3
12	24	27.0	15	2	PH1318 Ig heavy chain DJ
13	24	27.0	19	2	PK0062 beta-galactoside-b
14	23.5	26.4	16	2	S03532 Ig heavy chain J r
15	23.5	26.4	16	2	D49021 Ig heavy chain J7
16	23	25.8	7	2	S57274 triacylglycerol 11
17	23	25.8	11	2	PH1343 Ig heavy chain DJ
18	23	25.8	12	2	I46922 gene Bcl2 protein
19	23	25.8	14	2	PH1639 Ig H chain V-D-J r
20	23	25.8	15	2	A56786 plimeloyl-coA synth
21	23	25.8	15	2	A45103 7 alpha-hydroxy-4-
22	23	25.8	16	2	A59046 alpha-conotoxin MI
23	23	25.8	18	2	S43958 Ig mu chain V regi
24	23	25.8	17	2	S03531 neurotoxin Tx3 - s
25	22.5	25.3	17	2	S03531 Ig heavy chain J5
26	22	24.7	6	2	A61068 locustakinin V - mlg
27	22	24.7	8	2	JS0315 leucokinin VI - Ma
28	22	24.7	8	2	JS0316 leucokinin VII - M
29	22	24.7	8	2	JS0317

30	22	24.7	9	2	A24244	adipokinetic hormo
31	22	24.7	11	2	A34662	Achaticin cardio-ex
32	22	24.7	12	2	S26553	T-cell receptor be
33	22	24.7	12	2	S26548	T-cell receptor be
34	22	24.7	13	2	A61514	glutathione transf
35	22	24.7	15	2	PH1619	Ig H chain V-D-J r
36	22	24.7	16	2	PH1634	Ig H chain V-D-J r
37	22	24.7	17	2	A37823	dihydrolipeamide S
38	22	24.7	18	2	S33645	hypothetical prote
39	22	24.7	18	2	I52623	hypothetical prote
40	22	24.7	19	2	S62864	toxin VI - Tlytus
41	22	24.7	19	2	PH1756	T cell receptor al
42	22	24.7	8	2	US0318	leucokinin VIII -
43	22	24.7	10	2	S51912	hemagglutinin - in
44	22	24.7	10	2	PH0923	T-cell receptor be
45	22	24.7	10	2	S53789	neuropeptide Rec-H
46	22	24.7	12	2	PH1635	Ig H chain V-D-J r
47	22	24.7	13	2	S36668	hypothetical prote
48	22	24.7	14	2	PH0747	T-cell receptor be
49	22	24.7	17	2	I57941	beta 3-adrenergic
50	22	24.7	17	2	A36824	tachyplestin I - ho
51	22	24.7	17	2	JX0125	Ig heavy chain J r
52	22	24.7	17	2	S03533	gamma-crystallin I
53	22	24.7	17	2	PS0384	gamma-crystallin I
54	22	24.7	18	2	H75063	gamma-crystallin I
55	22	24.7	19	2	B60894	serine proteinase
56	22	24.7	19	2	JX0124	Ig heavy chain DJ
57	22	24.7	19	2	S12268	Ig heavy chain J r
58	22	24.7	20	2	C61570	T-cell receptor be
59	22	24.7	20	2	PC2084	T antigen variant
60	22	24.7	20	2	PH1341	Ig H chain V-D-J r
61	22	24.7	15	2	S10388	somatostatin - sli
62	22	24.7	16	2	PS0383	somatostatin I - c
63	22	24.7	9	2	PH0942	somatostatin I - E
64	22	24.7	11	2	PH1375	somatostatin I - s
65	22	24.7	11	2	PH1376	nitrogenase (EC 1.
66	22	24.7	13	2	PH1599	Ig H chain V-D-J r
67	22	24.7	14	2	I39753	Ig heavy chain CDR
68	22	24.7	14	2	PH1628	Ig H chain V-D-J r
69	22	24.7	14	2	A60842	hypothetical TCR3/
70	22	24.7	14	2	A60840	hypothetical prote
71	22	24.7	14	2	S00172	N4-(beta-N-acetyl
72	22	24.7	14	2	I39753	ribosomal protein
73	22	24.7	14	2	PH1628	Ig heavy chain CDR
74	22	24.7	16	2	PH0296	probable flagellar
75	22	24.7	16	2	PH1640	gamma-crystallin V
76	22	24.7	16	4	I79565	lipoprotein AcfP p
77	22	24.7	16	4	A33171	monocyte chemotact
78	22	24.7	18	2	S49026	Ig heavy chain V r
79	22	24.7	19	2	PH0244	Ig heavy chain J1
80	22	24.7	19	2	A61144	T-cell receptor ga
81	22	24.7	20	2	B60894	isotocin - common
82	22	24.7	20	2	D50894	T-cell receptor be
83	22	24.7	20	2	B39108	T-cell receptor be
84	22	24.7	20	2	I67551	glutathione transf
85	22	24.7	15	2	S26791	alpha-conotoxin Im
86	22	24.7	18	2	S03528	glucan endo-1,3-be
87	22	24.7	8	2	A38887	T-cell receptor de
88	22	24.7	9	2	A61364	Ig H chain V-D-J r
89	22	24.7	9	2	PH0562	collecting duct wa
90	22	24.7	9	2	PH0562	glycerolaldehyde-3-p
91	22	24.7	10	2	A57309	leucokinin III -
92	22	24.7	12	1	S71868	T-cell receptor al
93	22	24.7	12	1	A53709	hemagglutinin - in
94	22	24.7	12	2	S28215	T-cell receptor be
95	22	24.7	12	2	B49033	glutathione transf
96	22	24.7	12	2	PH1587	Ig H chain V-D-J r
97	22	24.7	13	2	B28810	collecting duct wa
98	22	24.7	13	2	I51905	glycerolaldehyde-3-p
99	22	24.7	14	2	S54344	leucokinin III -
100	22	24.7	15	2	PH0779	T-cell receptor al

ALIGNMENTS

RESULT 1

S57567
T cell receptor V-J junctional alpha chain region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
C:Accession: S57567
R:Burrows, S.R.; Sillis, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argact, V.P.
Submitted to the EMBL Data Library, June 1995
A:Description: T cell receptor repertoire for a viral epitope in humans is diversified
A:Reference number: S57494
A:Accession: S57567
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <BUR>
A:Cross-references: EMBL:Z49949; NID:g887470; PIDN:CAA90220.1; PID:g887471
C:Keywords: T-cell receptor

Query Match 30.3%; Score 27; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NSWG 5
: |||
Db 5 NSWG 8

RESULT 2

S29635
jacalin beta chain - Artocarpus tonkinensis
C:Species: Artocarpus tonkinensis
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S29635
R:Noguchi, L.D.; Brillard, M.; Hoebeke, J.
Biochim. Biophys. Acta 1156, 219-222, 1993
A:Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-kD
A:Reference number: S29635; MUID:93152601; PMID:8427879
A:Accession: S29635
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <NGO>

Query Match 30.3%; Score 27; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 9.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 LNSWGCK 7
: |||
Db 12 VGSWGAK 18

RESULT 3

S10386
Ig heavy chain J region (clone Re107) - little skate (fragment)
C:Species: Raja erinacea (little skate)
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Aug-1996
C:Accession: S10386
R:Harding, F.A.; Cohen, N.; Litman, G.W.
Nucleic Acids Res. 18, 1015-1020, 1990
A:Title: Immunoglobulin heavy chain gene organization and complexity in the skate, Raja
A:Reference number: S08462; MUID:90192082; PMID:2107524
A:Accession: S10386
A:Molecule type: DNA
A:Residues: 1-15 <HAR>
A:Cross-references: EMBL:X15124
C:Keywords: heterotetramer; immunoglobulin

Query Match 29.8%; Score 26.5; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 8.6e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

OY 1 LNSWGCKRIICYS 15
: ||| : |||
Db 2 LDYWG-ESTMYTTS 15

RESULT 4

PC4416
ERBB kinase activator gamma, brain and thymus - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Dec-1997 #sequence_revision 10-Dec-1997 #text_change 02-Aug-2002
C:Accession: PC4416
R:Hisashiyama, S.; Horikawa, M.; Yamada, K.; Ichino, N.; Nakano, N.; Nakagawa, T.; Mi
J. Biochem. 122, 675-680, 1997
A:Title: A novel brain-derived member of the epidermal growth factor family that inte
A:Reference number: J05700; MUID:98006324; PMID:9348101
A:Accession: PC4416
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-16 <HIG>
A:Cross-references: DBJ:D89998; NID:q2605635; PIDN:BAA23347.1; PID:q2605636
A:Experimental source: PC-12 cell
A:Comment: This protein is a member of the epidermal growth factor family. It is func
ating the differentiation of MDA-MB-453 cells.
C:Superfamily: human ERBB kinase activator alpha, brain and thymus; EGF homology

Query Match 29.2%; Score 26; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 LNSWGCKG 8
: |||
Db 9 INOLSCKG 16

RESULT 5

EMSMAN
ancovenin - Streptomyces sp. (strain A647P-2)
C:Species: Streptomyces sp.
C:Date: 12-May-1994 #sequence_revision 19-May-1994 #text_change 19-May-1994
C:Accession: A61284
R:Nakamiya, T.; Ueki, Y.; Shiba, T.; Kido, Y.; Motoki, Y.
Tetrahedron Lett. 26, 665-668, 1985
A:Title: The structure of ancovenin, a new peptide inhibitor of angiotensin I convert
A:Reference number: A61284
A:Accession: A61284
A:Molecule type: protein
A:Residues: 1-19 <NAK>
C:Superfamily: cinnamycin precursor
C:Keywords: antibiotic; lantibionine
F:1-18/Cross-link: (2S,3S,6R)-3-methyl-lantibionine (Cys-Thr) #status experimental
F:4-14/Cross-link: sn-(2S,6R)-lantibionine (Ser-Cys) #status experimental
F:5-11/Cross-link: (2S,3S,6R)-3-methyl-lantibionine (Cys-Thr) #status experimental
F:6/Modified site: dehydroalanine (Ser) #status experimental

Query Match 29.2%; Score 26; DB 1; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 SWGCKG 8
: |||
Db 11 TWSCDG 16

RESULT 6

S24570
Ig heavy chain J region - channel catfish
C:Species: Ictalurus punctatus (channel catfish)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S24570
R:Wilson, M.R.
Submitted to the EMBL Data Library, March 1992
A:Reference number: S24570
A:Accession: S24570

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-17 <MIL>
 A:Cross-references: EMBL:X65182; NID:964015; PIRN:CMA46293.1; PID:964016
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotetramer; Immunoglobulin

Query Match 28.7% Score 25.5; DB 2; Length 17;
 Best Local Similarity 50.0%; Pred. No. 1.4e+03;
 Matches 6; Conservative 1; Mismatches 4; Indels 1; Gaps 1;
 Oy 4 WCGKGRICYS 15
 Db 7 WG-KGTAVTVTS 17

RESULT 7
 A58700
 actgarden [validated] - "Actinoplanes liguriae"
 N:Alternate names: gardimycin
 C:Species: "Actinoplanes liguriae"
 A:Note: ATCC 31048
 C:Date: 16-Jan-1998 #sequence_revision 23-Jan-1998 #text_change 15-Sep-2000
 C:Accession: A58700; A58701
 R:Zimmermann, N.; Jung, G.
 Eur. J. Biochem. 246, 809-819, 1997
 A:Title: The three-dimensional solution structure of the lantibiotic murein-biosynthesis
 A:Reference number: A58700; MUID:97363218; PMID:9219543
 A:Accession: A58700
 A:Molecule type: protein
 A:Residues: 1-19 <ZIM>
 A:Note: the assignment of residues 1-Ser and 6-Cys are based on model studies
 R:Zimmermann, N.; Metzger, J.W.; Jung, G.
 Eur. J. Biochem. 228, 786-797, 1995
 A:Title: The tetracyclic lantibiotic actagardine. (1)H-NMR and (13)C-NMR assignments and
 A:Reference number: A58701; MUID:9555286; PMID:7737178
 A:Accession: A58701
 A:Molecule type: protein
 A:Residues: 'X', 2-5, 'X', 7-19 <ZIM>
 A:Note: residues 1 and 6, indicated as 'X', are serine and cysteine, but which is in whi
 R:Zimmermann, N.; Jung, G.
 submitted to the Brookhaven Protein Data Bank, May 1997
 A:Reference number: A67976; PDB:1AJ1
 A:Content: annotation: conformation and cross-link assignments by (1)H- and (13)C-NMR,
 C:Superfamily: unassigned lantibiotic-containing peptides
 C:Keywords: antibiotic; lantibiotic
 F:1-6/Cross-link: sn-(2S,6R)-lanthionine (Ser-Cys) #status experimental
 F:7-12/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Thr-Cys) #status experimental
 F:9-17/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Thr-Cys) #status experimental
 F:14-19/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Thr-Cys) #status experimental

Query Match 28.7% Score 25.5; DB 2; Length 19;
 Best Local Similarity 31.2%; Pred. NO. 1.5e+03;
 Matches 5; Conservative 2; Mismatches 4; Indels 5; Gaps 1;
 Oy 2 NSMGCK-----GRIC 12
 Db 2 SGWVCTLTIECTVTC 17

RESULT 8
 PH1306
 Ig heavy chain DJ region (clone C96-100) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: PH1306
 R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph
 A:Reference number: PH1302; MUID:95094761; PMID:1460419
 A:Accession: PH1306
 A:Molecule type: DNA

A:Residues: 1-14 <MAS>
 C:Keywords: heterotetramer; Immunoglobulin

Query Match 28.1% Score 25; DB 2; Length 14;
 Best Local Similarity 60.0%; Pred. No. 1.4e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Oy 11 ICYTS 15
 Db 4 VCYYT 8

RESULT 9
 S02381
 probable membrane antigen CLI - human herpesvirus 4 (fragment)
 C:Species: human herpesvirus 4, Epstein-Barr virus
 C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 08-Oct-1999
 C:Accession: S02381
 R:Walls, D.; Gannon, F.
 EMBO J. 7, 1191-1196, 1988
 A:Title: The expression of novel antigens from the Epstein-Barr virus large internal
 A:Reference number: S02381; MUID:88296424; PMID:2841116
 A:Accession: S02381
 A:Molecule type: DNA
 A:Residues: 1-15 <MAL>
 A:Cross-references: EMBL:X07814; NID:959167; PIRN:CMA30673.1; PID:9930013
 C:Keywords: membrane protein; surface antigen

Query Match 28.1% Score 25; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. NO. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 4 WCKGR 9
 Db 6 WCKGR 11

RESULT 10
 S03530
 Ig heavy chain J region (JH-4) - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 21-Jul-2000
 C:Accession: S03530
 R:Schwager, J.; Grosberger, D.; du Pasquier, L.
 EMBO J. 7, 2409-2415, 1988
 A:Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xe
 A:Reference number: S01158; MUID:89052653; PMID:2903824
 A:Accession: S03530
 A:Molecule type: DNA
 A:Residues: 1-14 <SCH>
 A:Cross-references: EMBL:X14918; NID:964805; PIRN:CMA33043.1; PID:91334657

Query Match 27.5% Score 24.5; DB 2; Length 14;
 Best Local Similarity 41.7%; Pred. NO. 1.7e+03;
 Matches 5; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
 Oy 4 WCKGRICYS 15
 Db 4 WG-QGTLVTVTS 14

RESULT 11
 A59173
 nuclease Bhl (EC 3.1.-.-) - Basidiobolus haptosporius (fragment)
 C:Species: Basidiobolus haptosporius
 C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
 C:Accession: A59173
 R:Desai, N.; Shankar, V.
 submitted to the Protein Sequence Database, February 2000
 A:Description: Single-strand-specific, guanylic acid preferential nuclease from Basid
 A:Reference number: A59173
 A:Accession: A59173
 A:Status: preliminary

A:Molecule type: protein
 A:Residues: 1-10 <DES>
 A:Cross-references: single-strand-specific nuclease
 A:Note: extracellular, single-strand-specific nuclease
 C:Keywords: hydrolase

Query Match 27.0%; Score 24; DB 2; Length 10;
 Best Local Similarity 37.5%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 4 WGCKGRIT 11
 |||
 DB 1 WGLIHL 8

RESULT 12

PH1318 Ig heavy chain DJ region (clone C527-121) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C:Accession: PH1318

R:Masserman, R.; Gallit, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph

A:Reference number: PH1302; MUID:93094761; PMID:1460419

A:Accession: PH1318

A:Molecule type: DNA

A:Residues: 1-15 <NMS>

C:Keywords: heterotrimer; immunoglobulin

Query Match 27.0%; Score 24; DB 2; Length 15;

Best Local Similarity 75.0%; Pred. No. 2.1e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 11 ICYT 14
 |||
 DB 2 VCYT 5

RESULT 13

PH0062

beta-galactoside-binding lectin - Caenorhabditis elegans (fragment)

C:Species: Caenorhabditis elegans

C:Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 26-May-2000

C:Accession: PX0062

R:Hirabayashi, J.; Satoh, M.; Ohyama, Y.; Kasai, K.

J. Biochem. 111, 553-555, 1992

A:Title: Purification and characterization of beta-galactoside-binding proteins from Ca

A:Reference number: PX0062; MUID:92348337; PMID:1639749

A:Accession: PX0062

A:Molecule type: protein

A:Residues: 1-19 <HR>

C:Superfamily: lactose-binding lectin L-36

Query Match 27.0%; Score 24; DB 2; Length 19;

Best Local Similarity 50.0%; Pred. No. 2.5e+03;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 NSWCKGR 9
 |||
 DB 10 NEMGNER 17

RESULT 14

S03532 Ig heavy chain J region (JH-7) - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 20-Jun-2000

C:Accession: S03532

R:Schwager, J.; Grossberger, D.; du Pasquier, L.

EMBO J. 7, 2409-2415, 1988

A:Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenop

A:Reference number: S01158; MUID:89052653; PMID:2903824

A:Accession: S03532

A:Molecule type: DNA

A:Residues: 1-16 <SCH>

A:Cross-references: EMBL:X14918; NID:q64805; PIDN:CAN33046.1; PID:q1334660

A:Note: the authors translated the codon AAC for residue 1 as Asp

C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 26.4%; Score 23.5; DB 2; Length 16;
 Best Local Similarity 41.7%; Pred. No. 2.6e+03;
 Matches 5; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

OY 4 WGCKGRITCYTS 15
 |||
 DB 6 WG-QGTWTVTS 16

RESULT 15

D49021 Ig heavy chain J7 region - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999

C:Accession: D49021

R:Haite, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.

J. Exp. Med. 171, 1721-1737, 1990

A:Title: Eleven distinct V-H gene families and additional patterns of sequence variat

A:Reference number: A47624; MUID:90237760; PMID:2110243

A:Accession: D49021

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-16 <HAT>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

Query Match 26.4%; Score 23.5; DB 2; Length 16;
 Best Local Similarity 41.7%; Pred. No. 2.6e+03;
 Matches 5; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

OY 4 WGCKGRITCYTS 15
 |||
 DB 6 WG-QGTWTVTS 16

RESULT 16

S57274 triacylglycerol lipase (EC 3.1.1.3) - Psychrobacter immobilis (fragment)

C:Species: Psychrobacter immobilis

C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 03-Nov-1995

C:Accession: S57274

R:Arpigny, J.L.; Feller, G.; Gerday, C.

Biochim. Biophys. Acta 1283, 103, 1995

A:Title: Corrigendum to 'Cloning, sequence and structural features of a lipase from t

A:Reference number: S57274; MUID:95359197; PMID:7632728

A:Accession: S57274

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-7 <ARP>

A:Cross-references: EMBL:X67712

C:Keywords: carboxylic ester hydrolase

Query Match 25.8%; Score 23; DB 2; Length 7;
 Best Local Similarity 57.1%; Pred. No. 2.8e+05;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 WGCKGRIT 10
 |||
 DB 1 WGDKQDI 7

RESULT 17

PH143 Ig heavy chain DJ region (clone C100-91) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

A:Reference number: S01158; MUID:89052653; PMID:2903824

A:Accession: PH143

R:Wasserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rivera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DHJ joining in young children with B precursor lymphoma
A:Reference number: PH1302; MUID:93094761; PMID:11460419
A:Accession: PH1343
A:Molecule type: DNA
A:Residues: 1-11 <MAS>
C:Keywords: heterotetramer; Immunoglobulin

Query Match 25.8%; Score 23; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNSMG 5
| : | |
Db 4 LDNMG 8

RESULT 18
I46922
gene Bc1a protein - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-Nov-1999
C:Accession: I46922
R:Ellis, S.A.; Braem, K.A.; Morrison, W.I.
Immunogenetics 37, 49-56, 1992
A:Title: Transmembrane and cytoplasmic domain sequences demonstrate at least two expressed
A:Reference number: I46921; MUID:93052564; PMID:11428011
A:Accession: I46922
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-12 <EL>
A:Cross-references: GB:547738; MID:9258999; PIDN:AMB23972.1; PID:9259000
C:Genetics:
A:Gene: Bc1a

Query Match 25.8%; Score 23; DB 2; Length 12;
Best Local Similarity 70.0%; Pred. No. 2.5e+03;
Matches 7; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

OY 5 GCKGRICYT 14
| | | | | |
Db 1 GCKGRIT--YT 8

RESULT 19
I9 H chain V-D-J region (clone B-1ess 230) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1639
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-1ess mice
A:Reference number: PH1580; MUID:9301609; PMID:8315387
A:Accession: PH1639
A:Molecule type: DNA
A:Residues: 1-14 <LEV>
A:Experimental source: bone marrow pre-B lymphocyte
C:Keywords: immunoglobulin

Query Match 25.8%; Score 23; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 8 GRITCY 13
| : | | |
Db 7 GVLLCY 12

RESULT 20
A56786
p1me1oy1-coa synthase - Bacillus sphaericus (fragment)

C:Species: Bacillus sphaericus
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 18-Aug-1995
C:Accession: A56786
R:Ploix, O.; Souliard, P.; Marguet, A.; Gloeckler, R.; Lemoine, Y.
Biochem. J. 287, 685-690, 1992
A:Title: Investigation of the first step of biotin biosynthesis in Bacillus sphaericus
A:Reference number: A56786; MUID:93075017; PMID:1445232
A:Accession: A56786
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <PILO>
A:Experimental source: Bacillus sphaericus protein overexpressed in Escherichia coli
A:Note: sequence extracted from NCBI backbone (NCBIP:117639)
C:Genetics:
A:Gene: b1ow
C:Keywords: biotin biosynthesis; homodimer

Query Match 25.8%; Score 23; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 10 IICYT 14
| | | | |
Db 2 LICYS 6

RESULT 21
A45103
7 alpha-hydroxy-4-cholesten-3-one 12 alpha-hydroxylase, cytochrome P450 12a1pha, HCO
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 03-Mar-1995
C:Accession: A45103
R:Shida, H.; Noshito, M.; Okuda, K.; Coon, M.J.
J. Biol. Chem. 267, 21319-21323, 1992
A:Title: Purification and characterization of 7 alpha-hydroxy-4-cholesten-3-one 12 alpha
A:Reference number: A45103; MUID:93016066; PMID:1400444
A:Accession: A45103
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <ISH>
A:Experimental source: liver microsomes
A:Note: sequence extracted from NCBI backbone (NCBIP:116791)

Query Match 25.8%; Score 23; DB 2; Length 15;
Best Local Similarity 37.5%; Pred. No. 3e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 4 MGCKGRIT 11
| | | | |
Db 3 MGLLGALL 10

RESULT 22
A59046
alpha-conotoxin MII - cone shell (Conus magus)
C:Species: Conus magus (magus cone)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: A59046
R:Cartier, G.E.; Yoshikami, D.; Gray, W.R.; Luo, S.; Olivera, B.M.; McIntosh, J.M.
J. Biol. Chem. 271, 7522-7528, 1996
A:Title: A new alpha-conotoxin which targets alpha3beta2 nicotinic acetylcholine rec
A:Reference number: A59046; MUID:96205934; PMID:8631783
A:Accession: A59046
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <CAR>
C:Superfamily: alpha-conotoxin
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu
F:1-16/Product: alpha-conotoxin MII #status experimental <MAR>
F:2-8,3-16/Disulfide bonds: #status experimental
F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 25.8%; Score 23; DB 2; Length 16;

Best Local Similarity 33.3%; Pred. No. 3.1e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 5 GCKGRICV 13
||
1 GGCSPVCH 9

RESULT 23

S43958
Ig mu chain V region (clone 2) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C:Accession: S43958
R:Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, K.;
Nucleic Acids Res. 22, 1389-1393, 1994
A:Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.
A:Reference number: S43956; MUID:94248036; PMID:8190629
A:Accession: S43958
A:Molecule type: DNA
A:Residues: 1-18 <WAG>
C:Keywords: immunoglobulin

Query Match 25.8%; Score 23; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNSWG 5
::|||
Db 12 VDSWG 16

RESULT 24

C39305
neurotoxin TX3 - spider (Phoneutria nigriventer) (fragment)
C:Species: Phoneutria nigriventer
C>Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 07-Feb-1997
C:Accession: C39305
R:Rezende, Jr., L.; Cordeiro, M.N.; Oliveira, E.B.; Diniz, C.R.
Toxicon 29, 1225-1233, 1991
A:Title: Isolation of neurotoxic peptides from the venom of the 'armed' spider Phoneutria
A:Reference number: A39305; MUID:92196803; PMID:1801316
A:Accession: C39305
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-19 <REZ>
C:Keywords: neurotoxin

Query Match 25.8%; Score 23; DB 2; Length 19;
Best Local Similarity 80.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 GCKGR 9
||
Db 1 GCIGR 5

RESULT 25

S03531
Ig heavy chain J5 region - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 20-Jun-2000
C:Accession: S03531; C49021
R:Schwager, J.; Grosberger, D.; du Pasquier, L.
EMBO J. 7, 2409-2415, 1988
A:Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenopus
A:Reference number: S01158; MUID:89052653; PMID:2903824
A:Accession: S03531
A:Molecule type: DNA
A:Residues: 1-17 <SCH>
A:CROSS-references: EMBL:X14918; NID:964805; PIDN:CAA33044.1; PID:q134658
R:Haire, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.
J. Exp. Med. 171, 1721-1737, 1990

A:Title: Eleven distinct V-H gene families and additional patterns of sequence variation
A:Reference number: A47624; MUID:90237760; PMID:2110243

A:Accession: C49021
A:Status: Preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 3-17 <HA1>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 25.3%; Score 22.5; DB 2; Length 17;
Best Local Similarity 41.7%; Pred. No. 3.9e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

OY 4 WCKGRICVTS 15
||
Db 7 WCA-GTMTVTS 17

RESULT 26

A61068
locustakinin - migratory locust
C:Species: Locusta migratoria (migratory locust)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Dec-1995
C:Accession: A61068
R:Schoofs, L.; Holman, G.M.; Proost, P.; Van Damme, J.; Hayes, T.K.; De Loof, A.
Regul. Pept. 37, 49-57, 1992
A:Title: Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation,
A:Reference number: A61068; MUID:92262851; PMID:1585017
A:Accession: A61068
A:Molecule type: protein
A:Residues: 1-6 <SCH>
C:Keywords: amidated carboxyl end; cephalomyotropic peptide; neuropeptide
F:6/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 24.7%; Score 22; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NSWG 5
|||
Db 3 SSWG 6

RESULT 27

JS0315
leucokinin V - Madeira cockroach
C:Species: Leucophaea maderae (Madeira cockroach)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C:Accession: JS0315
R:Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 27-30, 1987
A:Title: Isolation, primary structure, and synthesis of leucokinin V and VI: myotrop
A:Reference number: JS0315
A:Accession: JS0315
A:Molecule type: protein
A:Residues: 1-8 <HOL>
C:Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile
C:Keywords: amidated carboxyl end; cephalomyotropic peptide
F:8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 24.7%; Score 22; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NSWG 5
|||
Db 5 SSWG 8

RESULT 28

JS0316
leucokinin VI - Madeira cockroach
C:Species: Leucophaea maderae (Madeira cockroach)

C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C:Accession: JS0316

R:Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 27-30, 1987

A:Title: Isolation, primary structure, and synthesis of leucokinin V and VI: myotropic

A:Reference number: JS0315
A:Accession: JS0316

A:Molecule type: protein

A:Residues: 1-8 <HOL>

C:Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile act

C:Keywords: amidated carboxyl end; cephalomyotropic peptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 24.7%; Score 22; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NSMG 5
DB 5 HSMG 8

RESULT 29

JS0317

leucokinin VII - Madeira cockroach

C:Species: Leucophaea maderae (Madeira cockroach)

C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000

C:Accession: JS0317

R:Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 31-34, 1987

A:Title: Isolation, primary structure and synthesis of leucokinin VII and VIII: the fln

A:Reference number: JS0317

A:Molecule type: protein

A:Residues: 1-8 <HOL>

C:Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile act

C:Keywords: amidated carboxyl end; cephalomyotropic peptide

F:8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 24.7%; Score 22; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NSMG 5
DB 5 SSMG 8

RESULT 30

A24244

adipokinetin hormone - bollworm

N:Alternate names: Hez-AKH

C:Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)

C:Date: 31-Mar-1988 #sequence_revision 23-Mar-1995 #text_change 31-Oct-1997

C:Accession: A24244

R:Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway
Biochem. Biophys. Res. Commun. 135, 622-628, 1986

A:Title: Isolation and primary structure of a peptide from the corpora cardiaca of Helic

A:Reference number: A24244; MUID:86186794; PMID:3964263

A:Molecule type: protein

A:Residues: 1-9 <JAF>

C:Superfamily: adipokinetin hormone

C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 24.7%; Score 22; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NSMG 5

DB :|||
6 SSMG 9

Search completed: June 5, 2003, 09:00:02
Job time : 18 secs

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OM protein - protein search, using sw model

Run on: June 5, 2003, 08:58:43 ; Search time 11 Seconds

(without alignments)
56.559 Million cell updates/sec

Title: US-09-605-573a-69_COPY_12-26

Perfect score: 89

Sequence: 1 LNSWCKGRITCYTS 15

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 1147

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	30.3	8	1	LCR1_LEUMA
2	27	30.3	8	1	LCR3_LEUMA
3	27	30.3	8	1	LEC1_ARTIN
4	26	29.2	19	1	DURC_STRSP
5	26	29.2	19	1	LANC_STRSQ
6	25.5	28.7	19	1	LANA_ACTLG
7	23	25.8	12	1	CXL3_CONMR
8	23	25.8	16	1	CXL2_CONMA
9	23	25.8	19	1	TX3_PHONI
10	22	24.7	6	1	LCR1_LOCM1
11	22	24.7	8	1	LCR4_LEUMA
12	22	24.7	8	1	LCR5_LEUMA
13	22	24.7	8	1	LCR6_LEUMA
14	22	24.7	8	1	LCR7_LEUMA
15	22	24.7	8	1	LCR8_LEUMA
16	22	24.7	11	1	CEP1_ACHFU
17	22	24.7	15	1	LCR_DROME
18	22	24.7	18	1	GOME_ACAGO
19	22	24.7	19	1	SCX6_TITRA
20	22	24.7	20	1	LEC3_ARTIN
21	21	23.6	8	1	LCR8_LEUMA
22	21	23.6	17	1	TAC1_TACGI
23	21	23.6	17	1	TAC3_TACGI
24	20	22.5	11	1	CXL1_CONMR
25	20	22.5	12	1	CXL4_CONMR
26	20	22.5	13	1	CXL5_CONMR
27	20	22.5	14	1	CXL6_CONMR
28	20	22.5	14	1	CXL7_CONMR
29	20	22.5	15	1	CXL8_CONMR
30	19	21.3	9	1	ISOT_CYPCA
31	19	21.3	9	1	OXYT_RATCL
32	19	21.3	11	1	TIN4_HOPTI
33	19	21.3	12	1	CXAL_CONIM

34	19	21.3	14	1	SAP2_ARBP
35	19	21.3	14	1	SCR3_LEUQU
36	19	21.3	17	1	ROBR_CHITE
37	19	21.3	17	1	TPIS_PINPS
38	19	21.3	18	1	PPM1_LIMPO
39	19	21.3	18	1	PPM2_LIMPO
40	19	21.3	19	1	CXR_CONTU
41	19	21.3	20	1	CUDE_VERCH
42	19	21.3	20	1	THIO_CANFA
43	18	20.2	10	1	HTF1_ROMMI
44	18	20.2	10	1	HTF2_CARMO
45	18	20.2	10	1	HTF3_CARMO
46	18	20.2	10	1	HTF4_CARMO
47	18	20.2	13	1	TEM1_RANTE
48	18	20.2	14	1	CAL1_CALGI
49	18	20.2	15	1	TAL1_TREPR
50	18	20.2	15	1	UC19_MAIZE
51	18	20.2	17	1	CXMA_CONPE
52	17.5	19.7	17	1	CXMB_CONPE
53	17	19.1	18	1	HSTB_ECOLI
54	17	19.1	8	1	ACT1_THUAL
55	17	19.1	10	1	BPP8_BOTIN
56	17	19.1	10	1	HTF_NAUCI
57	17	19.1	10	1	HTF_TNABT
58	17	19.1	10	1	LABA_JATMU
59	17	19.1	13	1	MLA_AMOCA
60	17	19.1	13	1	MLA_CAMDR
61	17	19.1	13	1	NO40_VICSA
62	17	19.1	14	1	MAST_VESBA
63	17	19.1	15	1	CXAX2_CONLU
64	17	19.1	15	1	CXAX3_CONLU
65	17	19.1	15	1	CKGG_CARCR
66	17	19.1	15	1	UC08_MAIZE
67	17	19.1	16	1	CXAL1_CONAL
68	17	19.1	16	1	CXAX3_CONAL
69	17	19.1	17	1	FLAW_AZOCH
70	17	19.1	17	1	RANR_RANRU
71	17	19.1	18	1	MLB_HORSE
72	17	19.1	18	1	MLB_SCYCA
73	17	19.1	20	1	FLAW_AZOVI
74	17	19.1	20	1	HOL1_FASHE
75	17	19.1	20	1	LEC2_MACPO
76	17	19.1	20	1	LEC3_MACPO
77	17	19.1	20	1	OMPL_ACRAC
78	16	18.0	9	1	OXYA_SCYCA
79	16	18.0	9	1	OXYA_SQVAC
80	16	18.0	9	1	OXYT_BURE
81	16	18.0	9	1	OXYT_CYPCA
82	16	18.0	9	1	OXYT_OCTVU
83	16	18.0	9	1	OXYT_RABIT
84	16	18.0	9	1	OXYV_SQVAC
85	16	18.0	10	1	GLEW_HUMAN
86	16	18.0	11	1	TINI_HOPTI
87	16	18.0	12	1	CXST_CONTE
88	16	18.0	12	1	V14K_MSSV
89	16	18.0	13	1	TEMA_RANTE
90	16	18.0	13	1	YRNP_PROLU
91	16	18.0	14	1	LPW_CITFR
92	16	18.0	14	1	LPW_SALTY
93	16	18.0	14	1	UHA2_CANFA
94	16	18.0	14	1	UN37_CLOPA
95	16	18.0	15	1	ALIS_MANSE
96	16	18.0	15	1	KLOM_LUNTE
97	16	18.0	15	1	UC23_MAIZE
98	16	18.0	16	1	FIBA_MUSVI
99	16	18.0	16	1	FIBA_RABIT
100	16	18.0	16	1	PA2_NAUSP

ALIGNMENTS

RESULT 1

RESULT 2

ID	LECK3_LEUMA	STANDARD:	PRT:	8 AA.
AC	P21142;			
DT	01-MAY-1991 (Rel. 18, Created)			
DT	01-MAY-1991 (Rel. 18, Last sequence update)			
DT	01-MAY-1991 (Rel. 18, Last annotation update)			
DE	Leucokinin I (L-I).			
OS	Leucophaea maderae (Madeira cockroach).			
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;			
OC	Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;			
OC	Blaberoidea; Blaberidae; Leucophaea.			
OX	NCBI_TaxID=6988;			
RN	[1]			
RP	SEQUENCE, AND SYNTHESIS.			
RC	TISSUE-Head;			
RA	Holman G.M., Cook B.J., Nachman R.J.;			
RT	"Isolation, primary structure and synthesis of two neuropeptides			
RT	from Leucophaea maderae: members of a new family of			
RT	Cephalomyotroptins."			
RL	Comp. Biochem. Physiol. 84C:205-211(1986).			
CC	-1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE			
CC	ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).			
CC	-1- SIMILARITY: TO THE OTHER LEUCOKININS.			
KW	Neuropeptide; Amidation.			
FT	MOD.RES 8			
SO	SEQUENCE 8 AA; 893 MW; DC635B449CDC76A CRC64;			

Query Match 30.3%; Score 27; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3

ID	LECI_ARTIN	STANDARD:	PRT:	20 AA.
AC	P18671;			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	01-NOV-1990 (Rel. 35, Last annotation update)			
DE	Agglutinin beta-1 chain (Jacalin beta-1 chain).			
OS	Artocarpus integrifolia (Jack fruit) (Artocarpus integrifolia).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eucosids I; Rosales; Moraceae; Artocarpus.			
OX	NCBI_TaxID=3490;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE-Seed;			
RA	MEDLINE=99206218; PubMed=2705782;			
RT	Young N.M., Johnston R.A.Z., Szabo A.G., Watson D.C.;			
RT	"Homology of the D-galactose-specific lectins from Artocarpus			
RT	integrifolia and MacLura pomifera and the role of an unusual small			
RT	polypeptide subunit."			
RL	Arch. Biochem. Biophys. 270:596-603(1989).			
CC	[2]			
CC	SEQUENCE.			
CC	MEDLINE=92287028; PubMed=1599414;			
RA	Manhanta S.K., Sankar S., Prasad Rao N.V.S.A.V., Swamy M.J.;			
RT	"Primary structure of a Thomsen-Friedenreich antigen-specific lectin,			
RT	Jacalin [Artocarpus integrifolia (jack fruit) agglutinin]. Evidence			
RT	for the presence of an internal repeat."			
RL	Biochem. J. 284:95-101(1992).			
CC	[3]			
CC	SEQUENCE.			
CC	MEDLINE=93152601; PubMed=8427879;			
RA	Ngoc L.D., Brillard M., Hoebeke J.;			
RT	"The alpha- and beta-subunits of the jacalins are cleavage products			
RT	from a 17-kDa precursor."			
RL	Biochim. Biophys. Acta 1156:219-222(1993).			
CC	[4]			
CC	X-RAY CRYSTALLOGRAPHY (2.43 ANGSTROMS).			
RA	MEDLINE=9626349; PubMed=8673603;			
RT	Sakaranarayanan R., Sekar S., Banerjee R., Sharma V., Sutolija A.;			
RT	Vijayan M.;			
RL	"A novel mode of carbohydrate recognition in jacalin, a Moraceae			
RL	plant lectin with a beta-prism fold."			
RL	Nat. Struct. Biol. 3:596-603(1996).			
CC	-1- FUNCTION: D-GALACTOSE-SPECIFIC LECTIN, BINDS THE T-ANTIGEN			
CC	STRUCTURE GAL-BETA1-3-GALNAc (THOMSEN-FRIEDENREICH-ANTIGEN-			
CC	SPECIFIC LECTIN).			
CC	-1- FUNCTION: POTENT AND SELECTIVE STIMULANT OF DISTINCT T- AND B-CELL			
CC	FUNCTIONS. SHOWS A UNIQUE ABILITY TO SPECIFICALLY RECOGNIZE IGA-1			
CC	FROM HUMAN SERUM.			
CC	-1- SUBUNIT: Tetramer of four alpha chain associated with two or four			
CC	BETA CHAINS.			
CC	-1- SIMILARITY: TO THE OTHER AGGLUTININ BETA CHAINS.			
DR	PIR: S03983; S03983.			
DR	PIR: S29638; S29638.			
DR	PDB: 1JAC; 05-JUN-97.			
KW	Lectin; IGA-binding protein; 3D-structure.			
SO	SEQUENCE 20 AA; 2062 MW; 894AFC95F4DDE248 CRC64;			

Query Match 30.3%; Score 27; DB 1; Length 20;
 Best Local Similarity 57.1%; Pred. No. 2.2e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Query Match 30.3%; Score 27; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4

ID	DURC_STRCP	STANDARD:	PRT:	19 AA.
DT	01-MAY-1991 (Rel. 18, Created)			
DT	01-MAY-1991 (Rel. 18, Last sequence update)			
DT	01-MAY-1991 (Rel. 18, Last annotation update)			
DE	Leucokinin I (L-I).			
OS	Leucophaea maderae (Madeira cockroach).			
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;			
OC	Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;			
OC	Blaberoidea; Blaberidae; Leucophaea.			
OX	NCBI_TaxID=6988;			
RN	[1]			
RP	SEQUENCE, AND SYNTHESIS.			
RC	TISSUE-Head;			
RA	Holman G.M., Cook B.J., Nachman R.J.;			
RT	"Isolation, primary structure and synthesis of two additional neuropeptides			
RT	from Leucophaea maderae: members of a new family of			
RT	Cephalomyotroptins."			
RL	Comp. Biochem. Physiol. 84C:271-276(1986).			
CC	-1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE			
CC	ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).			
CC	-1- SIMILARITY: TO THE OTHER LEUCOKININS.			
KW	Neuropeptide; Amidation.			
FT	MOD.RES 8			
SO	SEQUENCE 8 AA; 910 MW; DC635B449C866DA CRC64;			

Query Match 30.3%; Score 27; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC P36503;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Lanthibiotic duramycin C.
 OS Streptomyces griseoliteus.
 OC Bacteria; Actinobacteria (class); Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 NCBI_TaxID=29306;
 RN (1)
 RN SEQUENCE.
 RC STRAIN=R2107;
 RX MEDLINE=91107436; PubMed=2125590;
 RA Friedenham A., Fendrich G., Markl F., Markl W., Gruner J.,
 RA Raschdorf F., Peter H.H.;
 RA "duramycins B and C, two new lanthionine containing antibiotics as
 RT inhibitors of phospholipase A2. Structural revision of duramycin and
 RT cinamycin.";
 RL J. Antibiot. 43:1403-1412(1990).
 RN (2)
 RN STRUCTURE BY NMR.
 RP Zimmermann N., Freund S., Friedenham A., Jung G.;
 RT "Solution structure of the lantibiotics duramycin B and C.";
 RL Eur. J. Biochem. 216:419-428(1993).
 CC -1- FUNCTION: ACTS AS INHIBITOR OF PHOSPHOLIPASE A2.
 CC -1- PTM: MATURATION OF LANTHIBIOTICS INVOLVES THE ENZYMIC CONVERSION OF
 CC THR, SER, AND CYS INTO DEHYDRATED AA AND THE FORMATION OF SULFIDE
 CC BRIDGES. THIS IS FOLLOWED BY THE MEMBRANE TRANSLOCATION AND
 CC CLEAVAGE OF THE MODIFIED PRECURSOR.
 CC -1- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTHIBIOTICS.
 KW Antibiotic; Bacteriocin; Lanthibiotic.
 FT MOD_RES 4 4
 FT MOD_RES 6 6
 FT MOD_RES 11 11
 FT MOD_RES 18 18
 FT MOD_RES 19 19
 FT THIOETH 1 1
 FT THIOETH 4 4
 FT THIOETH 5 5
 FT THIOETH 11 11
 SQ SEQUENCE 19 AA; 2007 MW; E2404ECE3F95286A CRC64;
 Query Match 29.2%; Score 26; DB 1; Length 19;
 Best Local Similarity 50.0%; Pred. No. 3.1e+02;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 3 SWCKG 8
 DB 11 TWSGCG 16
 RESULT 5
 LANC_STRSQ STANDARD; PRT; 19 AA.
 AC P38655;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Lanthibiotic ancovenin.
 OS Streptomyces sp. (strain A647P-2).
 OC Bacteria; Actinobacteria (class); Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 NCBI_TaxID=1931;
 RN (1)
 RN SEQUENCE.
 RA Makamaya T., Ueki Y., Shiba T., Kido Y., Motoki Y.;
 RA "The structure of ancovenin, a new peptide inhibitor of angiotensin I

RT converting enzyme.";
 RL Tetrahedron Lett. 26:665-668(1985).
 CC -1- FUNCTION: ACTS AS INHIBITOR OF ANGIOTENSIN I CONVERTING ENZYME.
 CC -1- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTHIBIOTICS.
 DR PIR; A61284; EWSMAN.
 KW Antibiotic; Bacteriocin; Lanthibiotic.
 FT MOD_RES 4 4
 FT MOD_RES 6 6
 FT MOD_RES 11 11
 FT MOD_RES 18 18
 FT MOD_RES 19 19
 FT THIOETH 1 1
 FT THIOETH 4 4
 FT THIOETH 5 5
 FT THIOETH 11 11
 SQ SEQUENCE 19 AA; 2033 MW; F434299E2736286A CRC64;
 Query Match 29.2%; Score 26; DB 1; Length 19;
 Best Local Similarity 50.0%; Pred. No. 3.1e+02;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 3 SWCKG 8
 DB 11 TWSGCG 16
 RESULT 6
 LANA_ACTIG STANDARD; PRT; 19 AA.
 AC P56650;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Lanthibiotic actagardine (Gardimycin).
 OS Actinoplanes ligulata.
 OC Bacteria; Actinobacteria (class); Actinobacteridae;
 OC Actinomycetales; Micromonosporineae; Micromonosporaceae;
 OC Actinoplanes.
 NCBI_TaxID=69484;
 RN (1)
 RN PRELIMINARY SEQUENCE, AND STRUCTURE BY NMR.
 RP MEDLINE=91008696; PubMed=2211371;
 RA Kettentrung J.K., Malabarida A., Vekey K., Cavallieri B.;
 RT "Sequence determination of actagardine, a novel lantibiotic, by
 RT homonuclear 2D NMR spectroscopy.";
 RL J. Antibiot. 43:1082-1088(1990).
 RN (2)
 RN SEQUENCE, AND STRUCTURE BY NMR.
 RP MEDLINE=95255286; PubMed=7737178;
 RA Zimmermann N., Metzger J.W., Jung G.;
 RT "The tetracyclic lantibiotic actagardine, 1H-NMR and 13C-NMR
 RT assignments and revised primary structure.";
 RL Eur. J. Biochem. 228:786-797(1995).
 RN (3)
 RN STRUCTURE BY NMR.
 RP MEDLINE=97363218; PubMed=9219543;
 RA Zimmermann N., Jung G.;
 RT "The three-dimensional solution structure of the lantibiotic murein-
 RT biosynthesis-inhibitor actagardine determined by NMR.";
 RL Eur. J. Biochem. 246:809-819(1997).
 CC -1- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST SOME GRAM-POSITIVE
 CC BACTERIA. HAS GOOD ANTISTREPTOCOCCAL ACTIVITY.
 DR PDB; 1AI1; 15-OCT-97.
 KW Antibiotic; Bacteriocin; Lanthibiotic; 3D-structure.
 FT MOD_RES 1 1
 FT MOD_RES 7 7
 FT MOD_RES 9 9
 FT MOD_RES 14 14
 FT MOD_RES 19 19
 FT THIOETH 1 1
 FT THIOETH 7 7
 FT THIOETH 9 9
 FT THIOETH 14 14
 FT THIOETH 19 19
 SQ SEQUENCE 19 AA; 1962 MW; 5C1391CBEB8765B3 CRC64;

Query Match 28.7%; Score 25.5; DB 1; Length 19;
 Best Local Similarity 31.2%; Pred. No. 3.7e+02;
 Matches 5; Conservative 2; Mismatches 4; Indels 5; Gaps 1;

OY 2 NSMCK-----GRITC 12
 : : : : :
 DB 2 SGWCTLTIECGTVIC 17

RESULT 7
 ID CXL3_CONMR STANDARD: PRT: 12 AA.
 AC P58809;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lambda-conotoxin CMrx.
 OS Conus marmoreus (Marble cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 NCBI_TaxID=42752;
 RX [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC TISSUE-Venom;
 RA Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,
 Seow K.T., Bay B.-H.; A new family of conotoxins with unique disulfide
 pattern and protein folding. Isolation and characterization from the
 venom of Conus marmoreus.
 RT J. Biol. Chem. 275:39516-39522(2000).
 RL -1- FUNCTION: Inhibits the neuronal noradrenaline transporter.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- MASS SPECTROMETRY: MM=1262.77; MW ERR=0.07; METHOD=Electrospray.
 CC -1- SIMILARITY: BELONGS TO THE CHI/LAMBDA-CONOTOXIN FAMILY.
 KW Neurotoxin; Toxin; Hydroxylation.
 FT DISULFID 3 12
 FT MOD.RES 11 11 HYDROXYLATION.
 FT SEQUENCE 12 AA; 1251 MW; 277AAE2422D5A2C8 CRC64;

Query Match 25.8%; Score 23; DB 1; Length 12;
 Best Local Similarity 50.0%; Pred. No. 6.2e+02;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 6 CKGRITCY 13
 : : : : :
 DB 3 CCGVSFCY 10

RESULT 8
 ID CXL2_CONMA STANDARD: PRT: 16 AA.
 AC P56636;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin MII (M2).
 OS Conus magus (Magus cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 NCBI_TaxID=6492;
 RX [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE-Venom;
 RA Carlier G.E., Yoshikami D., Gray W.R., Luo S., Olivera B.M.,
 McIntosh J.M.;
 RT "A new alpha-conotoxin which targets alpha3beta2 nicotinic
 acetylcholine receptors".
 RL J. Biol. Chem. 271:7522-7528(1996).

RN [2]
 RP STRUCTURE BY NMR.
 RX MEDLINE=98062282; PubMed=9398298;
 RA Shon K.-J., Koerber S.C., Rivier J.E., Olivera B.M., McIntosh J.M.;
 RT "Three-dimensional solution structure of alpha-conotoxin MII, an
 alpha3beta2 neuronal nicotinic acetylcholine receptor-targeted
 ligand".
 RT Biochemistry 36:15693-15700(1997).
 RL [3]
 RP STRUCTURE BY NMR.
 RX MEDLINE=99060038; PubMed=9843366;
 RA Hill J.M., Oomen C.J., Miranda L.P., Bingham J.-P., Alewood P.F.,
 Craik D.J.;
 RT "Three-dimensional solution structure of alpha-conotoxin MII by NMR
 spectroscopy: effects of solution environment on helicity".
 RL Biochemistry 37:15621-15630(1998).
 CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
 BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
 INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC
 ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-2 SUBUNITS. IT
 HAS AN ACTIVITY 2 TO 4 ORDERS OF MAGNITUDE LESS POTENT ON OTHER
 NACHR SUBUNIT COMBINATIONS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- SIMILARITY: BELONGS TO THE A SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
 FAMILY.
 DR PDB: 1MTI; 21-OCT-98.
 DR PDB: 1M2C; 13-JAN-99.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Antidation; 3D-structure.
 FT DISULFID 2 8
 FT MOD.RES 16 16 AMINATION.
 FT SEQUENCE 16 AA; 1716 MW; 282AEF190166CAF9 CRC64;

Query Match 25.8%; Score 23; DB 1; Length 16;
 Best Local Similarity 33.3%; Pred. No. 8.1e+02;
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 5 GCKGRITCY 13
 : : : : :
 DB 1 GCCSNPCH 9

RESULT 9
 ID TX3_PHONI STANDARD: PRT: 19 AA.
 AC P31010;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neurotoxin TX3 (Fragment).
 OS Phoneutria nigriventer (Brazilian armed spider).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Araneomorphae; Entelegynae; Lycosoidae; Ctenidae; Phoneutria.
 NCBI_TaxID=6918;
 RX [1]
 RP SEQUENCE.
 RC TISSUE-Venom;
 RA Rezende L. Jr., Cordeliro M.N., Oliveira E.B., Diniz C.R.;
 RT "Isolation of neurotoxic peptides from the venom of the 'armed'
 spider Phoneutria nigriventer".
 RL Toxicon 29:1225-1233(1991).
 CC -1- FUNCTION: ANTAGONIST OF L-TYPE CALCIUM CHANNELS (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -1- SIMILARITY: BELONGS TO THE SPIDER TOXIN TX3 FAMILY.
 DR PIR: C39305; C39305.
 KW Calcium channel inhibitor; Toxin; Neurotoxin.
 FT NON-TER 19
 FT SEQUENCE 19 AA; 2244 MW; 3214E89CF10F7587 CRC64;

Query Match 25.8%; Score 23; DB 1; Length 19;
 Best Local Similarity 80.0%; Pred. No. 9.4e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0;

OY 5 GCKGR 9
 ||||
 1 CCKGR 5

RESULT 10
 LCK1_LOCMI STANDARD; PRT; 6 AA.
 AC P41491;

DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Locustakinin I.
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caellifera;
 AC Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;

RA de Loof A.;
 RA Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
 RA "Locustakinin, a novel myotropic peptide from locusta migratoria,
 RT isolation, primary structure and synthesis.";
 RL Regul. Pept. 37:49-57(1992).

CC -1- FUNCTION: MYOTROPIC PEPTIDE. MAY BE IMPORTANT IN THE STIMULATION
 OF ION TRANSPORT AND INHIBITION OF DIURETIC ACTIVITY IN MALPIGHIAN
 TUBULES.
 DR PTR: A61068; A61068.
 KM Neuropeptide; Amidation.
 FT MOD_RES 6
 SQ SEQUENCE 6 AA: 654 MW; 686365A5B9CDB000 CRC64;

Query Match 24.7%; Score 22; DB 1; Length 6;
 Best Local Similarity 75.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0;

OY 2 NSWG 5
 ||||
 3 SSWG 6

Db 3 SSWG 6

RESULT 11

LCK2_LEUMA STANDARD; PRT; 8 AA.
 ID LCK2_LEUMA
 AC P21141;

DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-MAY-1991 (Rel. 18, Last annotation update)

DE Leucokinin II (L-II).
 OS Leucophaea maderae (Madeira cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blaberoidea; Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;

RT [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE-Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;

RT "Isolation, primary structure and synthesis of two neuropeptides
 from Leucophaea maderae: members of a new family of
 Cephalomyotropicins.";
 RL Comp. Biochem. Physiol. 84C:205-211(1986).

CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 ACTIVITY OF COCKROACH PROPODEUM (HINDGUT).
 CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
 KM Neuropeptide; Amidation.

FT MOD_RES 8
 SQ SEQUENCE 8 AA: 852 MW; DC6365B1E9D5BDDA CRC64;

Query Match 24.7%; Score 22; DB 1; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0;

OY 2 NSWG 5
 ||||
 5 SSWG 8

RESULT 12
 LCK4_LEUMA STANDARD; PRT; 8 AA.
 ID LCK4_LEUMA
 AC P21143;

DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-MAY-1991 (Rel. 18, Last annotation update)

DE Leucokinin IV (L-IV).
 OS Leucophaea maderae (Madeira cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blaberoidea; Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;

RA [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE-Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;

RT "Primary structure and synthesis of two additional neuropeptides
 from Leucophaea maderae: members of a new family of
 Cephalomyotropicins.";
 RL Comp. Biochem. Physiol. 84C:271-276(1986).

CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 ACTIVITY OF COCKROACH PROPODEUM (HINDGUT).
 CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
 KM Neuropeptide; Amidation.
 FT MOD_RES 8
 SQ SEQUENCE 8 AA: 906 MW; DC6365B1E9D5BDDA CRC64;

Query Match 24.7%; Score 22; DB 1; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0;

OY 2 NSWG 5
 ||||
 5 SSWG 8

Db 5 SSWG 8

RESULT 13
 LCK5_LEUMA STANDARD; PRT; 8 AA.
 ID LCK5_LEUMA
 AC P19987;

DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Leucokinin V (L-V).
 OS Leucophaea maderae (Madeira cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blaberoidea; Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;

RT [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE-Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;

RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
 myotropic peptides of Leucophaea maderae.";
 RL Comp. Biochem. Physiol. 88C:27-30(1987).
 CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 ACTIVITY OF COCKROACH PROPODEUM (HINDGUT).
 CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.

DR PIR: JS0315; JS0315.
 KW Neuropeptide; Amidation.
 FT MOD.RES 8
 SQ SEQUENCE 8 AA; 784 MW; 736365A5B9C865B8 CRC64;

Query Match 24.7%; Score 22; DB 1; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NSWG 5
 : : :
 : : :
 Db 5 SSWG 8

RESULT 14
 LCK6_LEUMA STANDARD; PRT; 8 AA.

AC P19988;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Leucokinin VI (L-VI).
 OS Leucophaea maderae (Madeira cockroach).
 OS Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blaberidae; Blaberidae; Leucophaea.
 OX NCBI_TaxID=6986;
 RN [1]
 RP SEQUENCE.

RC TISSUE-Head; MEDLINE=87052651; PubMed=2877794;
 RX Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
 myotropic peptides of leucophaea maderae.";
 RL Comp. Biochem. Physiol. 88C:27-30(1987).
 CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 ACTIVITY OF COCKROACH PROTOPODEM (HINDGUT).
 CC -1- SIMILARITY: TO THE OTHER LEUCOKININS, AND TO MANDUCA SEXTA AND
 CC HELIOTHRIS ZEA ADIPOKINETIC HORMONE.
 DR PIR: JS0316; JS0316.
 KM Neuropeptide; Amidation.
 FT MOD.RES 1 8
 FT MOD.RES 8 AA; 935 MW; 906365B1E9D5A5A6 CRC64;

SQ SEQUENCE 8 AA; 935 MW; 906365B1E9D5A5A6 CRC64;
 Query Match 24.7%; Score 22; DB 1; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NSWG 5
 : : :
 : : :
 Db 5 HSWG 8

RESULT 15
 LCK7_LEUMA STANDARD; PRT; 8 AA.

AC P19989;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Leucokinin VII (L-VII).
 OS Leucophaea maderae (Madeira cockroach).
 OS Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blaberidae; Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE.

RC TISSUE-Head; Cook B.J., Nachman R.J.;
 RA Holman G.M., primary structure and synthesis of leucokinin VII and
 RT "Isolation, primary structure and synthesis of leucokinin VII and
 RT VIII: the final members of this new family of cephalomyotrophic

RT peptides isolated from head extracts of leucophaea maderae.";
 RL Comp. Biochem. Physiol. 88C:31-34(1987).
 CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 CC ACTIVITY OF COCKROACH PROTOPODEM (HINDGUT).
 CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
 DR PIR: JS0317; JS0317.
 KW Neuropeptide; Amidation.
 FT MOD.RES 8
 SQ SEQUENCE 8 AA; 866 MW; D6365A5B9C9C76A CRC64;

Query Match 24.7%; Score 22; DB 1; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NSWG 5
 : : :
 : : :
 Db 5 SSWG 8

RESULT 16
 CEPL_ACHFU STANDARD; PRT; 11 AA.

AC P22790;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Cardio-excitatory peptide-1 (ACEP-1).
 OS Achatina fulica (Giant African snail).
 OS Achatina fulica (Giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 OC Achatinacea; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE.

RC STRAIN=Ferrussac; TISSUE=Heart atrium;
 RX MEDLINE=90011261; PubMed=2322251;
 RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;
 RT "A novel cardio-excitatory peptide isolated from the atria of the
 RT African giant snail, Achatina fulica".
 RL Biochem. Biophys. Res. Commun. 167:777-783(1990).
 CC -1- FUNCTION: POTENTIATES THE BEAT OF THE VENTRICLE, AND HAS ALSO
 CC EXCITATORY ACTIONS ON THE PENIS RETRACTOR MUSCLE, THE BUCCAL
 CC MUSCLE AND THE IDENTIFIED NEURONS CONTROLLING THE BUCCAL MUSCLE
 CC MOVEMENT OF ACHATINA.
 CC -1- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.
 DR PIR: A34662; A34662.
 KM Hormone; Amidation.
 FT MOD.RES 11 11
 FT MOD.RES 11 AA; 1305 MW; 82D6D5B9C7741365 CRC64;

SQ SEQUENCE 11 AA; 1305 MW; 82D6D5B9C7741365 CRC64;
 Query Match 24.7%; Score 22; DB 1; Length 11;
 Best Local Similarity 57.1%; Pred. No. 8.4e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 SWSGCR 9
 : : :
 : : :
 Db 4 SWRPGR 10

RESULT 17
 LCK_DROME STANDARD; PRT; 15 AA.

AC P81829;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Leucokinin (DLK).
 OS Drosophila melanogaster (Fruit fly).
 OS Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachytera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE.

RP SEQUENCE.
 RC TISSUE-Neurosecretory cell;
 RX MEDLINE=20044845; PubMed=1054744;
 RA Terhaz S., O'Connell F.C., Pollock V.P., Kean L., Davies S.A.,
 RA Ventrata J.A., Dow J.A.T.;
 RT Isolation and characterization of a leucokinin-like peptide of
 RT Drosophila melanogaster;
 RT J. Exp. Biol. 202;3667-3676(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Gelniker S.E., Agdayani A., Arcalina T.T., Baxter E., Blazek R.G.,
 RA Butenkov C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
 RA Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
 RA Houston K.A., Hummel S.R., Karia K., Kearney L., Kim E., Lee B.,
 RA Lewis S., Li P., Lomolan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
 RA Nixon K., Paclet J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
 RA Sethi H., Smit E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
 RA Zleran L.L., Rubin G.M.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: ACTS THROUGH INTRACELLULAR CALCIUM IN MALPIGHIAN TUBULE
 CC STELLATE CELLS TO RAISE CHLORIDE CONDUCTANCE.
 CC -----
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 CC or send an email to license@sdb.ch).
 CC -----
 CC DR EMBL: AC006496; NOT_ANNOTATED_CDS.
 CC DR Flybase: FBgn028418; Leucokinin.
 CC KW Neuropeptide; Amidation.
 CC FT MOD_RES 15 15
 CC SQ SEQUENCE 15 AA; 1743 MW; 4793A08E251C9525 CRC64;
 OY Query Match 24.7%; Score 22; DB 1; Length 15;
 Db Best Local Similarity 75.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 2 NSMG 5
 Db 12 HSWG 15
 RESULT 18
 GOME_ACAGO STANDARD; PRT; 18 AA.
 AC P82358;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE GomeSLn.
 OS Acanthoscurria gomesiana.
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Mygalomorphae; Theraphosidae; Acanthoscurria.
 OX NCBI_TaxID=115339;
 RN [1]
 RP SEQUENCE, MASS SPECTROMETRY, ACTIVITY, TISSUE SPECIFICITY, AMIDATION,
 RP AND DISULFIDE BONDS.
 RC TISSUE-Hemocyte;
 RX MEDLINE=20517902; PubMed=10942757;
 RA Silva P.J., Jr., Daffre S., Bullet P.;
 RT "Isolation and characterization of gomesin, an 18-residue cysteine-
 RT rich defense peptide from the spider Acanthoscurria gomesiana
 RT hemocytes with sequence similarities to horseshoe crab antimicrobial
 RT peptides of the tachyplesin family";
 RL J. Biol. Chem. 275;33464-33470(2000).
 CC -1- FUNCTION: ACTIVE AGAINST SEVERAL GRAM-POSITIVE BACTERIA SUCH AS
 CC BACILLUS SPP., STAPHYLOCOCCUS SPP AND E. FACALIS, SEVERAL GRAM-
 CC NEGATIVE BACTERIA SUCH AS E. COLI, K. PNEUMONIAE, P. AERUGINOSA AND
 CC SALMONELLA SPP., FILAMENTOUS FUNGI SUCH AS N. CRASSA, T. VIRIDAE

CC AND YEASTS SUCH AS C. ALBICANS. IT IS ACTIVE AGAINST THE PARASITE
 CC L. AMAZONENSIS AS WELL. IT SHOWS HEMOLYTIC ACTIVITY.
 CC -1- TISSUE SPECIFICITY: HEMOCYTES.
 CC -1- MASS SPECTROMETRY: MW=2270.4; METHOD=MALDI.
 KW Amidation; Antibiotic; Fungicide; Hemolysis.
 FT MOD_RES 1 1
 FT MOD_RES 18 18
 FT DISULFID 2 15
 FT DISULFID 6 11
 SQ SEQUENCE 18 AA; 2293 MW; 25ED49784908913 CRC64;
 OY Query Match 24.7%; Score 22; DB 1; Length 18;
 Db Best Local Similarity 75.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 6 CKGR 9
 Db 15 CKGR 18
 RESULT 19
 SCX6_TITBA STANDARD; PRT; 19 AA.
 AC P56610;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Toxin TbrX-VI (Fragment).
 OS Tityus bahiensis (Brazilian scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Buthoidea; Buthidae; Tityus.
 OX NCBI_TaxID=50343;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Venom;
 RX MEDLINE=96190713; PubMed=8611151;
 RA Becerril B., Corona M., Coronas F.I., Zamudio F.,
 RA Calderon-Aranda E.S., Fletcher P.L., Jr., Martin B.M., Possant L.D.;
 RT "Toxic peptides and genes encoding toxin gamma of the Brazilian
 RT scorpions Tityus bahiensis and Tityus stigmurus";
 RL Biochem. J. 313;753-760(1996).
 CC -1- FUNCTION: NOT TOXIC IN MICE.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
 CC ALPHA-TOXIN SUBFAMILY.
 CC DR Interpro: IPR002061; Scorpion_toxinL.
 CC DR Pfam: PF00537; toxin_3; 1.
 CC DR NON_TER 19 19
 CC SQ SEQUENCE 19 AA; 2151 MW; 3535A2F1E5E67D14 CRC64;
 OY Query Match 24.7%; Score 22; DB 1; Length 19;
 Db Best Local Similarity 44.4%; Pred. No. 1.4e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 2; Gaps 1;
 OY 5 GCKGRITCY 13
 Db 11 GCKR-LTGF 17
 RESULT 20
 LEC3_ARTIN STANDARD; PRT; 20 AA.
 ID LEC3_ARTIN
 AC P18673;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-JUL-1993 (Rel. 26, Last annotation update)
 DE Agglutinin beta-3 chain (Jaccalin beta-3 chain).
 OS Artocarpus integer (Jack fruit) (Artocarpus integrifolia).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosida I; Rosales; Moraceae; Artocarpus.
 OX NCBI_TaxID=3490;
 RN [1]

RP SEQUENCE.
RC TISSUE-Seed:
RX MEDLINE-89206218; PubMed-2705782;
RA Young N.M., Johnston R.A.Z., Szabo A.G., Watson D.C.;
RT "Homology of the D-galactose-specific lectins from *Artocarpus integrifolia* and *MacLura pomifera* and the role of an unusual small polypeptide subunit.";
RT Arch. Biochem. Biophys. 270:596-603(1989).
RN [2]
RP SEQUENCE.
RX MEDLINE-92287028; PubMed-1599414;
RA Mahanta S.K., Sanker S., Prasad Rao N.V.S.A.V., Swamy M.J.,
RT "Primary structure of a Thomsen-Friedenreich-antigen-specific lectin, jacalin [*Artocarpus integrifolia* (jack fruit) agglutinin]. Evidence for the presence of an internal repeat.";
RL Blochem. J. 284:95-101(1992).
CC -1- FUNCTION: D-GALACTOSE-SPECIFIC LECTIN, BINDS THE T-ANTIGEN-STRUCTURE GAL-BETA1-3-GALNAc (THOMSEN-FRIEDENREICH-ANTIGEN-SPECIFIC LECTIN).
CC -1- FUNCTION: POTENT AND SELECTIVE STIMULANT OF DISTINCT T- AND B-CELL FUNCTIONS. SHOWS A UNIQUE ABILITY TO SPECIFICALLY RECOGNIZE IGA-1 FROM HUMAN SERUM.
CC -1- SUBUNIT: TETRAMER OF FOUR ALPHA CHAIN ASSOCIATED WITH TWO OR FOUR BETA CHAINS.
CC -1- SIMILARITY: TO THE OTHER AGGLUTININ BETA CHAINS.
CC PIR: S03985; S03985.
DR Lectin; Iga-binding protein.
KW SEQUENCE 20 AA; 2058 MW; 894AFC989B0E212 CRC64;
SQ

Query Match 24.7%; Score 22; DB 1; Length 20;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 MGCK 7
Db 15 WGAH 18

RESULT 21
LCR8_LEUMA STANDARD; PRT; 8 AA.
AC P19990;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Leucokinin VIII (L-VIII).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID-6988;
RN [1]
RP SEQUENCE.
RC TISSUE-Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of leucokinin VII and VIII: the final members of this new family of cephalomyotropic peptides isolated from head extracts of *Leucophaea maderae*.";
RL Comp. Biochem. Physiol. 88C:31-34(1987).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODERM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
DR Neuropeptide; Amidation.
FT MOD.RES 8
SO SEQUENCE 8 AA; 902 MW; 736365AB9CADD8 CRC64;

Query Match 23.6%; Score 21; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 SWG 5

Db 6 SWG 8
RESULT 22
TACL_TACGI STANDARD; PRT; 17 AA.
AC P23684;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-NOV-1991 (Rel. 32, Last annotation update)
DE Tachyplesin I.
OS Tachyplesus gigas (Southeast Asian horseshoe crab), and
OS Carcinoscopus rotundicauda (Southeast Asian horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Tachyplesus.
OX NCBI_TaxID-6852, 6848;
RN [1]
RP SEQUENCE.
RC SPECIES-T. gigas, and C. rotundicauda;
RX MEDLINE-91035357; PubMed-2229025;
RA Muta T., Fujimoto T., Nakajima H., Iwanaga S.;
RT "Tachyplesins isolated from hemocytes of Southeast Asian horseshoe crabs (*Carcinoscopus rotundicauda* and *Tachyplesus gigas*): identification of a new tachyplesin, tachyplesin III, and a processing intermediate of its precursor.";
RL J. Biochem. 108:261-266(1990).
CC -1- SIMILARITY: BELONGS TO THE TACHYPLESIN/POLYPHEMUSIN FAMILY.
DR PIR: A38824; A38824.
KW Antibiotic; Amidation.
FT DISULFID 3
FT MOD.RES 7 12
FT 17 17
SQ SEQUENCE 17 AA; 2269 MW; E9E09BD9D2923C94 CRC64;
Query Match 23.6%; Score 21; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 RITCY 13
Db 9 RIGCY 13

RESULT 23
TAC3_TACGI STANDARD; PRT; 17 AA.
AC P18252;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Tachyplesin III.
OS Tachyplesus gigas (Southeast Asian horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Tachyplesus.
OX NCBI_TaxID-6852;
RN [1]
RP SEQUENCE.
RC MEDLINE-91035357; PubMed-2229025;
RX Muta T., Fujimoto T., Nakajima H., Iwanaga S.;
RT "Tachyplesins isolated from hemocytes of Southeast Asian horseshoe crabs (*Carcinoscopus rotundicauda* and *Tachyplesus gigas*): identification of a new tachyplesin, tachyplesin III, and a processing intermediate of its precursor.";
RL J. Biochem. 108:261-266(1990).
CC -1- FUNCTION: SIGNIFICANTLY INHIBITS THE GROWTH OF GRAM-NEGATIVE AND GRAM-POSITIVE BACTERIA.
CC -1- TISSUE SPECIFICITY: HEMOCYTES.
CC -1- SIMILARITY: BELONGS TO THE TACHYPLESIN/POLYPHEMUSIN FAMILY.
DR PIR: JX0125; JX0125.
KW Antibiotic; Amidation.
FT DISULFID 3
BY SIMILARITY. 16

FT DISULFID 7 12 BY SIMILARITY.
MOD.RES 17 17 AMIDATION.
SQ SEQUENCE 17 AA; 2241 MW; E9E08CE9D2923C94 CRC64;
Query Match 23.6%; Score 21; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 RICCY 13
1 1 1 1
DB 9 RGICY 13

RESULT 24

CK1L_CONMR STANDARD; PRT; 11 AA.
AC P58807;

DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lambda-conotoxin CM7VIA.
OS Conus marmoreus (Marble cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conidae; Conus.
OX NCBI_TaxID=42752;

RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.

RX TISSUE-Venom.
MEDLINE=20564325; PubMed=10988292;

RA Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,
Sew K.T., Bay B.-H.;

RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide
pattern and protein folding. Isolation and characterization from the
venom of Conus marmoreus.";
RL J. Biol. Chem. 275:39516-39522(2000).
CC -1- FUNCTION: Inhibits the neuronal noradrenergic transporter.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=1237.93; MW_ERR=0.21; METHOD=Electrospray.
CC -1- SIMILARITY: BELONGS TO THE CHI/LAMBDA-CONOTOXIN FAMILY.
KW Neurotoxin; Toxin; Hydroxylation.

FT DISULFID 3 11
FT MOD_RES 10 10 HYDROXYLATION.
SQ SEQUENCE 11 AA; 1226 MW; 277AAC60B23B58 CRC64;

Query Match 22.5%; Score 20; DB 1; Length 11;
Best Local Similarity 37.5%; Pred. No. 1.8e+03;

Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 6 CKGRICY 13
1 1 1 1
DB 2 CCGYKICH 9

RESULT 25

TIN3_HOPTI STANDARD; PRT; 12 AA.
AC P82653;

DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tigeritin-3.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;

RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.

RC TISSUE-Skin;

RA PubMed=11031261;
Purna Sai K., Jagannathan M.V., Vairaman M., Raju N.P.,

RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigeritins: novel antimicrobial peptides from the Indian frog Rana
tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -1- FUNCTION: ANTI-BACTERIAL ACTIVITY AGAINST B. SUBTILIS, E. COLI,
S. AUREUS, M. LUTENS, P. PUTIDA AND S. CEREVISIAE.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: SKIN.
CC -1- MASS SPECTROMETRY: MW=1409; METHOD=MALDI.
KW Amphibian skin; Antibiotic; Amidation.
FT DISULFID 3 11
FT MOD_RES 12 12
SQ SEQUENCE 12 AA; 1411 MW; C0717DBED37605D CRC64;

Query Match 22.5%; Score 20; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 ICY 13
1 1 1 1
DB 10 ICY 12

RESULT 26

CK1L_CONMR STANDARD; PRT; 13 AA.
AC P58810;

DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lambda/chi-conotoxin MR1B (Chi-MR1B).
OS Conus marmoreus (Marble cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conidae; Conus.
OX NCBI_TaxID=42752;

RN [1]
RP SEQUENCE, SYNTHESIS, AND STRUCTURE BY NMR.
RC TISSUE-Venom;
MEDLINE=21419681; PubMed=11528421;

RA Sharpe I.A., Gehrmann J., Loughnan M.L., Thomas L., Adams D.A.,
Atkins A., Palant E., Craik D.J., Adams D.J., Alewood P.F.,
Lewis R.J.;

RT "Two new classes of conopeptides inhibit the alpha1-adrenoceptor and
noradrenergic transporter.";
RL Nat. Neurosci. 4:902-907(2001).

CC -1- FUNCTION: Inhibits the neuronal noradrenergic transporter.
CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- PTM: Exists in two forms, due to cis-trans isomerization at His-
11-Hyp-12.

CC -1- MASS SPECTROMETRY: MW=1393.52; METHOD=Electrospray.
CC -1- SIMILARITY: BELONGS TO THE CHI/LAMBDA-CONOTOXIN FAMILY.
DR PDB: 1IEO; 03-APR-02.

KW Neurotoxin; Toxin; Hydroxylation; 3D-structure.

FT DISULFID 4 13
FT MOD_RES 12 12 HYDROXYLATION.
SQ SEQUENCE 13 AA; 1382 MW; 277AAC376EAD2B58 CRC64;

Query Match 22.5%; Score 20; DB 1; Length 13;
Best Local Similarity 37.5%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 6 CKGRICY 13
1 1 1 1
DB 4 CCGYKICH 11

RESULT 27

SMS1_MYOSC STANDARD; PRT; 14 AA.
AC P20750;

DT 01-FEB-1991 (Rel. 17, Created)

01-FEB-1991 (Rel. 17, Last sequence update)
 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Somatostatin I.
 OS Myoxocephalus scorpius (Shorthorn sculpin) (Daddy sculpin),
 OS Oncorhynchus kisutch (coho salmon), and
 OS Anguilla anguilla (European freshwater eel).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
 OC Cottoidei; Cottidae; Myoxocephalus.
 OX NCBI_Taxid=8097, 8019, 7936;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=M. scorpius; TISSUE=Pancreas;
 RX MEDLINE=88029486; PubMed=2889597;
 RA Conlon J.M., Davis M.S., Falkner S., Thim L.;
 RT "Structural characterization of peptides derived from
 RT prosomatostatin I and II isolated from the pancreatic islets of two
 RT species of teleostean fish: the daddy sculpin and the flounder.";
 RL Eur. J. Biochem. 168:647-652(1987).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=O. kisutch; TISSUE=Pancreas;
 RX MEDLINE=87055212; PubMed=2877919;
 RA Pilsetskaya E.M., Pollock H.G., Rouse J.B., Hamilton J.W.,
 RA Kimmel J.R., Andrews P.C., Gorman A.;
 RT "Characterization of coho salmon (Oncorhynchus kisutch) islet
 RT somatostatins.";
 RL Gen. Comp. Endocrinol. 63:252-263(1986).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=A. anguilla; TISSUE=Pancreas;
 RX MEDLINE=89065329; PubMed=2904391;
 RA Conlon J.M., Deacon C.F., Hazen N., Henderson I.W., Thim L.;
 RT "Somatostatin-related and glucagon-related peptides with unusual
 RT structural features from the European eel (Anguilla anguilla).";
 RL Gen. Comp. Endocrinol. 72:181-189(1988).
 CC -1- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
 CC PIR: S00172; S00172.
 DR PIR: B60842; B60842.
 DR PIR: A60840; A60840.
 DR InterPro: IPR004250; Somatostatin.
 DR Pfam: PF03002; Somatostatin; 1.
 KW Hormone; Multigene family.
 FT DISULFID 3
 SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;
 Query Match 22.5%; Score 20; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SPECIES=A. mississippiensis; TISSUE=Stomach;
 RX MEDLINE=93324451; PubMed=8101369;
 RA Wang Y., Conlon J.M.;
 RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain
 RT and stomach of the alligator.";
 RL Peptides 14:573-579(1993).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=T. scripta;
 RX MEDLINE=90341082; PubMed=1974347;
 RA Conlon J.M., Hicks J.W.;
 RT "Isolation and structural characterization of insulin, glucagon and
 RT somatostatin from the turtle, Pseudemys scripta.";
 RL Peptides 11:461-466(1990).
 CC -1- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
 DR PIR: G60414; G60414.
 DR InterPro: IPR004250; Somatostatin.
 DR Pfam: PF03002; Somatostatin; 1.
 KW Hormone.
 FT DISULFID 3
 SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;
 Query Match 22.5%; Score 20; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 29
 CXIB CONBE STANDARD; PRT; 15 AA.
 ID CXIB CONBE
 AC P58624;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Conotoxin BxTxib.
 OS Conus betulinus (Beech cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_Taxid=89764;
 RN [1]
 RP SEQUENCE AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=20058566; PubMed=10591037;
 RA Chen J.-S., Fan C.-X., Hu K.-P., Wei K.-H., Zhong M.-N.;
 RT "Studies on conotoxins of Conus betulinus.";
 RL J. Nat. Toxins 8:341-349(1999).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- MASS SPECTROMETRY: MW=1642.5; METHOD=MALDI.
 CC -1- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS.
 KW Neurotoxin; Toxin.
 FT DISULFID 1 9 PROBABLE.
 FT DISULFID 2 12 PROBABLE.
 FT DISULFID 6 13 PROBABLE.
 SQ SEQUENCE 15 AA; 1650 MW; 3749BAF08E311337 CRC64;
 Query Match 22.5%; Score 20; DB 1; Length 15;
 Best Local Similarity 42.3%; Pred. No. 2.3e+03;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

RESULT 30
 ISOL_CYPCA
 OY 6 CKRITC 12
 DB 6 CHGVPC 12

ID ISOT_CYPCA STANDARD: PRT: 9 AA.
AC P42993;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Isotocin.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE
RC TISSUE=pituitary;
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Characterization of neurohypophyseal hormones from a fresh water bony
RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea
RT water bony fishs."
RL Comp. Biochem. Physiol. 14:245-254(1965).
CC -1- FUNCTION: ANTIDIURETIC HORMONE.
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A61364; A61364.
DR InterPro: IPR000981; Neurhyp_horm.
DR InterPro: IPR001230; Preuyl_site.
DR Pfam: PF00220; hormone4.1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KW hormone; Amidation.
FT DISUFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 969 MW; 17FF476EB455B04B CRC64;

Query Match 21.3%; Score 19; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.1e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 12 CYTS 15
DB 1 1
1 CYIS 4

Search completed: June 5, 2003, 08:59:40
Job time : 13 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 5, 2003, 08:58:43 ; Search time 27 Seconds
(without alignments)
114.471 Million cell updates/sec

Title: US-09-605-573a-69_COPY_12-26
Perfect score: 89
Sequence: 1 LNSWCKGRITCYTS 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 6395

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP viirus:*
16: SP bacteriap:*
17: SP archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	30.3	8	P82685	P82685 periplaneta
2	27	30.3	8	P82687	P82687 periplaneta
3	27	30.3	8	P82689	P82689 periplaneta
4	27	30.3	17	O9YQZ5	O9YQZ5 macaca fasc
5	27	30.3	10	O9S871	O9S871 artocarpus
6	25	28.1	15	O9S871	O9S871 artocarpus
7	25	28.1	15	O9S871	O9S871 artocarpus
8	24.5	27.5	20	O9S871	O9S871 artocarpus
9	24	27.0	12	O9S871	O9S871 artocarpus
10	24	27.0	17	O9S871	O9S871 artocarpus
11	24	27.0	20	O9S871	O9S871 artocarpus
12	24	27.0	20	O9S871	O9S871 artocarpus
13	24	27.0	20	O9S871	O9S871 artocarpus
14	24	27.0	20	O9S871	O9S871 artocarpus
15	23	25.8	10	O50032	O50032 mycobacteri
16	23	25.8	12	O31006	O31006 bos taurus

17	23	25.8	16	2	O45663	O45663 bacillus su
18	23	25.8	18	4	O96C65	O96C65 homo sapien
19	22	24.7	8	5	P82686	P82686 periplaneta
20	22	24.7	8	5	P82688	P82688 periplaneta
21	22	24.7	11	7	O77914	O77914 oreochromis
22	22	24.7	12	2	O56947	O56947 yersinia ps
23	22	24.7	13	8	O9XLI2	O9XLI2 rhizobium m
24	22	24.7	15	2	O69142	O69142 bentisita tab
25	22	24.7	16	11	O9OVU0	O9OVU0 streptococc
26	22	24.7	16	13	O9PVR0	O9PVR0 mus sp. mep
27	22	24.7	17	11	O6V157	O6V157 mus musculu
28	22	24.7	20	2	O93TWO	O93TWO neisseria m
29	22	24.7	12	12	O66202	O66202 transmissib
30	22	24.7	14	2	P83077	P83077 bacillus ce
31	22	24.7	15	6	O9R339	O9R339 gotilla gor
32	22	24.7	15	6	O9R339	O9R339 gotilla gor
33	22	24.7	15	6	O9R339	O9R339 gotilla gor
34	22	24.7	15	13	O9PS01	O9PS01 microgogon
35	22	24.7	16	2	O44543	O44543 anabaena va
36	22	24.7	16	2	O44543	O44543 anabaena va
37	22	24.7	17	2	O93S31	O93S31 rhodospiril
38	22	24.7	17	12	O85004	O85004 porcine res
39	22	24.7	18	4	O13665	O13665 homo sapien
40	22	24.7	18	17	O9UYK7	O9UYK7 pyrococcus
41	22	24.7	19	2	P74875	P74875 salmoneila
42	22	24.7	19	11	O06028	O06028 mus musculu
43	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
44	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
45	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
46	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
47	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
48	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
49	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
50	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
51	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
52	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
53	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
54	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
55	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
56	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
57	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
58	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
59	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
60	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
61	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
62	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
63	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
64	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
65	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
66	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
67	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
68	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
69	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
70	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
71	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
72	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
73	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
74	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
75	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
76	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
77	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
78	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
79	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
80	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
81	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
82	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
83	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
84	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
85	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
86	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
87	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
88	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu
89	22	24.7	20	13	O9PRR4	O9PRR4 scyllorhinu

ALIGNMENTS

PRELIMINARY; PRT; 8 AA.

Query Match	30.3%	Score 27	DB 5	Length 8
Best Local Similarity	100.0%	Pred. No.	6.7e+05	
Matches	4	Conservative	0	Mismatches 0
				Indels 0
				Gaps 0

PRELIMINARY;	PRT;	8 AA.
--------------	------	-------

AC 01-MAR-2001 (TREMBLrel. 16, created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
 DE kinin-3 (PEA-K-3).
 OS *Periplaneta americana* (American cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Orthoptera; Dictyoptera; Blattaria;
 CC Blattodea; Blattellidae; Periplaneta.
 OX NCBI_TaxId=6978;
 RN [1]
 RP SEQUENCE AND FUNCTION.
 RC TISSUE-CORPORA CARDIACA.
 RX MEDLINE=98010462; PubMed=9350979;
 RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
 RT Isolation and structural elucidation of eight kinins from the

QY 2 NSWG 5
|||

PRELIMINARY; PRT; 8 AA

Query Match	30.3%	Score	27	DB	5	Length	8
Best Local Similarity	100.0%	Pred. No.	6.7e+05				
Matches	4	Conservative	0	Mismatches	0	Indels	0

PRELIMINARY; PRT; 17 AA

AC 09/02/25;
 DT 01-MAY-2000 (TREMBLERel. 13, Created)
 DT 01-MAY-2000 (TREMBLERel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLERel. 21, Last annotation update)
 DE Glyceraldehyde 3-phosphate dehydrogenase (Fragment).
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; *
 CC Cercopithecoidea; Macaca.
 CX NCBI_TaxID=9541;
 RN [1]
 RN SEQUENCE.
 RP MEDLINE=96273610; PubMed=8690030;
 RX

RA Nicolas M.G., Fujiki K., Murayama K., Suzuki M.T., Mineki R.,
 RA Hayakawa M., Yoshikawa Y., Cho F., Kanai A.;
 RT "Studies on the mechanism of early onset macular degeneration in
 RT cynomolgus (Macaca fascicularis) monkeys. I. Abnormal concentrations
 of two proteins in the retina."
 RL Exp. Eye Res. 62:211-219(1996).
 CC -1- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + PHOSPHATE +
 CC NAD(+) = 3-PHOSPHO-D-GLYCEROL PHOSPHATE + NADH.
 CC -1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
 CC DEHYDROGENASE FAMILY.
 DR InterPro: IPR000173; GAP_dhdrogenase.
 DR Pfam: PF000044; gpdh.1.
 KW Glycolysis; NAD; Oxidoreductase.
 SQ SEQUENCE 17 AA; 1671 MW; 52CCDD0D1A98B3DAF CRC64;

Query Match 30.3%; Score 27; DB 6; Length 17;
 Best Local Similarity 36.4%; Pred. No. 6.4e+02;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 LNSMCKGRIT 11
 Db 7 VNGFGAIGRLV 17

RESULT 5
 09S8T1 PRELIMINARY; PRT; 20 AA.
 AC 09S8T1; 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Jacalin beta-subunit (Fragment).
 OS Artocarpus tonkinensis.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC Euphorbia; Rosales; Moraceae; Artocarpus.
 RX NCBI_Taxid=3492;
 RN 1
 RP MEDLINE=93152601; PubMed=8427879;
 RA Ngoc L.D., Brillard M., Hoebke J.;
 RT "The alpha- and beta-subunits of the jacalins are cleavage products
 RT from a 17-kDa precursor."
 RL Biochim. Biophys. Acta 1156:119-222(1993).
 FT NON_TER 1
 FT SEQUENCE 20 AA; 2131 MW; 894893667060E9FE CRC64;
 SQ

Query Match 30.3%; Score 27; DB 10; Length 20;
 Best Local Similarity 57.1%; Pred. No. 7.6e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 LNSMCK 7
 Db 12 VGSWGA 18
 ID 066543 PRELIMINARY; PRT; 15 AA.
 AC 066543; 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE Epitope C11 (16 AA) (Fragment)
 OS Human herpesvirus 4 (Epstein-Barr virus).
 CC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 CC Gammaherpesvirinae; Lymphocryptovirus.
 OX NCBI_Taxid=10376;
 RN 1
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=88296424; PubMed=2841116;

RA Walls D., Gannon F.;
 RT "The expression of novel antigens from the Epstein-Barr virus large
 RT internal repeat."
 RL EMBO J. 7:1191-1196(1988).
 DR EMBL: X07814; CAA30673.1; -.
 FT NON_TER 1
 FT SEQUENCE 15 AA; 1629 MW; 48BA5A4558C3266C CRC64;

Query Match 28.1%; Score 25; DB 12; Length 15;
 Best Local Similarity 66.7%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 4 WGCKGR 9
 Db 6 WGRKG 11

RESULT 7
 086576 PRELIMINARY; PRT; 15 AA.
 AC 086576; 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Coat protein (Fragment).
 OS Subterranean clover stunt virus.
 CC Viruses; ssDNA viruses; Nanovirus.
 OX NCBI_Taxid=36772;
 RN 1
 RP MEDLINE=93212590; PubMed=8460528;
 RA Chu P.W., Reese P., Qiu B.S., Waterhouse P.M., Gerlach W.L.;
 RT "Putative full-length clones of the genomic DNA segments of
 RT subterranean clover stunt virus and identification of the segment
 RT coding for the viral coat protein."
 RL Virus Res. 27:161-171(1993).
 DR EMBL: S57687; AAB25908.1; -.
 FT NON_TER 1
 FT SEQUENCE 15 AA; 1825 MW; 44D9CE497CD96FFD CRC64;
 SQ

Query Match 28.1%; Score 25; DB 12; Length 15;
 Best Local Similarity 80.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 WGCKG 8
 Db 5 WGRKG 9
 ID 09DE23 PRELIMINARY; PRT; 20 AA.
 AC 09DE23; 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE UORF2.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OX NCBI_Taxid=9031;
 RN 1
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20528616; PubMed=11073974;
 RA Kobayashi M., Yu R.T., Yasuda K., Umesono K.;
 RT "Cell-type-specific regulation of the retinoic acid receptor mediated
 RT by the orphan nuclear receptor TLX."
 RL Mol. Cell. Biol. 20:8731-8739(2000).
 DR EMBL: AF220160; AAG35363.1; -.
 DR InterPro: IPR000345; CytC_heme_bind.

DR InterPro: IPR003006; IG_MHC.
 DR PROSITE: PS00190; CYTOCHROME_C: UNKNOWN_1.
 DR PROSITE: PS00290; IG_MHC: UNKNOWN_1.
 SQ SEQUENCE 20 AA; 2261 MW; AA77738B0BEC482 CRC64;

Query Match 27.5%; Score 24.5; DB 13; Length 20;
 Best Local Similarity 26.7%; Pred. No. 2e+03;
 Matches 4; Conservative 5; Mismatches 3; Indels 3; Gaps 1;

OY 1 LNSMGCKRITCYTS 15
 | : : : : :
 Db 9 IQAFSC--VVCCHNS 20

RESULT 9

ID 012036 PRELIMINARY; PRT; 12 AA.
 AC 012036;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Caprine arthritis encephalitis virus (CAEV).
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11660;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97296261; PubMed=9151845;
 RA Turelli P., Guiguen F., Morne J.F., Vigne R., Querat G.;
 RT "oupsé-minus caprine arthritis-encephalitis virus is attenuated for
 RT pathogenesis and accumulates G-to-A substitutions.";
 RL J. Virol. 71:4522-4530(1997).
 DR EMBL: U81390; AAC57905.1; .
 FT NON PER 1
 SQ SEQUENCE 12 AA; 1398 MW; 8D24228CA3733455 CRC64;

Query Match 27.0%; Score 24; DB 15; Length 12;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 NSMGC 6
 | : : : :
 Db 6 NKWTC 10

RESULT 10

ID 006800 PRELIMINARY; PRT; 17 AA.
 AC 006800;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE N1780.
 GN LSM7 OR N1780 OR YNL147W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96287653; PubMed=8686380;
 RA Nasr F., Becam A.M., Herbert C.J.;
 RT "The sequence of 36.8 kb from the left arm of chromosome XIV reveals
 RT 24 complete open reading frames: 18 correspond to new genes, one of
 RT which encodes a protein similar to the human myotonic dystrophy
 RT kinase.";
 RL Yeast 12:169-175(1996).
 DR EMBL: X92517; CAA63292.1; .
 DR SGD: S0005091; LSM7.
 SQ SEQUENCE 17 AA; 2139 MW; BD7E9AFAFD754AF CRC64;

Query Match 27.0%; Score 24; DB 3; Length 17;

Best Local Similarity 60.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 11 ICYTS 15
 | : : : :
 Db 7 VCFTS 11

RESULT 11

ID 09XIW8 PRELIMINARY; PRT; 20 AA.
 AC 09XIW8;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Hypothetical protein.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Euphorbiaceae; Oryzae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Nagamura Y., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
 RT clone:P0681F10.";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB026295; BAA81863.1; .
 KW Hypothetical protein.
 SQ SEQUENCE 20 AA; 2312 MW; A5EE9C9093D159F9 CRC64;

Query Match 27.0%; Score 24; DB 10; Length 20;
 Best Local Similarity 80.0%; Pred. No. 2.4e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 CKGRT 10
 | : : : :
 Db 3 CSGRT 7

RESULT 12

ID 09S8EO PRELIMINARY; PRT; 20 AA.
 AC 09S8EO;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE Mannitol dehydrogenase (Fragment).
 OS Apium graveolens (Celery).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids II; Apiales; Apiaceae; Apium.
 OX NCBI_TaxID=4045;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95357413; PubMed=7630943;
 RA Scoop J.M., Williamson J.D., Conkling M.A., Pharr D.M.;
 RT "Purification of NAD-dependent mannitol dehydrogenase from celery
 RT suspension cultures.";
 RL Plant Physiol. 108:1219-1225(1995).
 SQ SEQUENCE 20 AA; 2361 MW; 0269A74330582DBF CRC64;

Query Match 27.0%; Score 24; DB 10; Length 20;
 Best Local Similarity 75.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NSMG 5
 | : : : :
 Db 16 NNMG 19

RESULT 13

090UK8
ID 090UK8 PRELIMINARY: PRT: 20 AA.
AC 090UK8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Alpha class glutathione S-transferase subunit 1B (BC 2.5.1.18) (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=96036981; PubMed=7485987;
RA Roullet P., Debrauer L., Tulliez J.;
RT Electrospray ionization-mass spectrometry as a tool for
RT characterization of glutathione S-transferase isozymes.;
RL Anal. Biochem. 229:304-312(1995).
DR HSP: P08263; IGUH.
SQ SEQUENCE 20 AA: 2421 MW: 949F405B7DA0B236 CRC64;

Query Match 27.0%; Score 24; DB 11; Length 20;
Best Local Similarity 33.3%; Pred. No. 2.4e+03;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 LNSGCKGRITC 12
Db 6 LHYFNAGRMGC 17

RESULT 14
084861
ID 084861 PRELIMINARY: PRT: 20 AA.
AC 084861;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hypothetical 2.2 kDa protein (Fragment).
OS unidentified human poliovirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.
NCBI_TaxID=40278;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87169734; PubMed=3031313;
RA Kuge S., Saito T., Nomoto A.;
RT "Primary structure of poliovirus defective-interfering particle
RT genomes and possible generation mechanisms of the particles.";
RL J. Mol. Biol. 192:473-487(1986).
DR EMBL: M30218; AAA66827.1; -.
KW Hypothetical protein.
FT NON_TER 1
FT SEQUENCE 20 AA: 2241 MW: 55D177D10BAF0FF9 CRC64;

Query Match 27.0%; Score 24; DB 12; Length 20;
Best Local Similarity 75.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NSWG 5
Db 7 NNWG 10

RESULT 15
050032
ID 050032 PRELIMINARY: PRT: 10 AA.
AC 050032;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBlrel. 01, Last annotation update)
DE U22669.

OS Mycobacterium leprae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith D.R.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA ROBISON K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U15182; AAA62975.1; -.
SQ SEQUENCE 10 AA: 1137 MW: 5F3F317B1EB455B7 CRC64;

Query Match 25.8%; Score 23; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 6 CKGR 10
Db 6 CEGRL 10

RESULT 16
031006
ID 031006 PRELIMINARY: PRT: 12 AA.
AC 031006;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Beta protein (Fragment).
GN BOFA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93052564; PubMed=1428011;
RA Ellis S.A., Braem K.A., Morrison W.I.;
RT "Transmembrane and cytoplasmic domain sequences demonstrate at least
RT two expressed bovine MHC class I loci.";
RL Immunogenetics 37:49-56(1992).
DR EMBL: S47738; AAB23972.1; -.
FT NON_TER 1
FT SEQUENCE 12 AA: 1306 MW: 6D9E2F805ABB5044 CRC64;

Query Match 25.8%; Score 23; DB 7; Length 12;
Best Local Similarity 70.0%; Pred. No. 2.2e+03;
Matches 7; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

OY 5 GCKGRITCYT 14
Db 1 GCKGRIT--YT 8

RESULT 17
045663
ID 045663 PRELIMINARY: PRT: 16 AA.
AC 045663;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE SacB levansucrase.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacilliales;
OC Bacillaceae; Bacillus.
NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MARBURG;

RX MEDLINE=85295507; PubMed=2993818;
 RA Steinmetz M., Le Cog D., Aymerich S., Gonzy-Treboul G., Gay P.;
 RT "The DNA sequence of the gene for the secreted Bacillus subtilis
 RT enzyme levanucrase and its genetic control sites.";
 RL Mol. Gen. Genet. 200:220-228(1985).
 DR EMBL; X02730; CAA26512.1; -;
 SQ SEQUENCE 16 AA; 1840 MW; E8CF83DC73713DA9 CRC64;

Query Match 25.8%; Score 23; DB 2; Length 16;
 Best Local Similarity 37.5%; Pred. No. 2.9e+03;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 6 CKGRITCY 13
 DB 2 CKGOSYVF 9

RESULT 18

AC 096C65; PRELIMINARY; PRT; 18 AA.

DT 01-DEC-2001 (TREMBLREL. 19, Created)

DT 01-DEC-2001 (TREMBLREL. 19, last sequence update)

DT 01-DEC-2001 (TREMBLREL. 19, last annotation update)

DE Hypothetical 2.1 kDa protein (Fragment).

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.

RC TISSUE=EYE;

RA Strausberg R.;

RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC014643; AAH14643.1; -;

KW Hypothetical protein.

FT NON TER 1
 SQ SEQUENCE 18 AA; 2105 MW; 3874A0D25D91AC9C CRC64;

Query Match 25.8%; Score 23; DB 4; Length 18;
 Best Local Similarity 60.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNSWG 5
 DB 1 LDANG 5

RESULT 19

P82686 PRELIMINARY; PRT; 8 AA.

DT 01-MAR-2001 (TREMBLREL. 16, Created)

DT 01-MAR-2001 (TREMBLREL. 16, last sequence update)

DT 01-MAR-2001 (TREMBLREL. 16, last annotation update)

DE Kinin-2 (PEA-K-2).

OS Periplaneta americana (American cockroach).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;

OC Blattodea; Blattidae; Periplaneta.

NCBI_TaxID=6978;

RP SEQUENCE, AND FUNCTION.

RC TISSUE=CORPORA CARDIACA;

RA MEDLINE=98010462; PubMed=9350979;

RA "Isolation and structural elucidation of eight kinins from the
 RT retrocerebral complex of the American cockroach, Periplaneta
 americana.";
 RL Regul. Pept. 71:199-205(1997).
 CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC -I- (MYOTROPIC ACTIVITY).
 CC -I- SIMILARITY: BELONGS TO THE KININ FAMILY.

KW Neuropeptide; Amidation.
 FT MOD_RES 8
 SQ SEQUENCE 8 AA; 856 MW; DC6365A5B9DBDDA CRC64;

Query Match 24.7%; Score 22; DB 5; Length 8;
 Best Local Similarity 75.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NSWG 5
 DB 5 SSWG 8

RESULT 20

P82688 PRELIMINARY; PRT; 8 AA.

DT 01-MAR-2001 (TREMBLREL. 16, Created)

DT 01-MAR-2001 (TREMBLREL. 16, last sequence update)

DT 01-MAR-2001 (TREMBLREL. 16, last annotation update)

DE Kinin-4 (PEA-K-4).

OS Periplaneta americana (American cockroach).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;

OC Blattodea; Blattidae; Periplaneta.

NCBI_TaxID=6978;

RP SEQUENCE, AND FUNCTION.

RC TISSUE=CORPORA CARDIACA;

RA MEDLINE=98010462; PubMed=9350979;

RA "Isolation and structural elucidation of eight kinins from the
 RT retrocerebral complex of the American cockroach, Periplaneta
 americana.";
 RL Regul. Pept. 71:199-205(1997).
 CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC -I- (MYOTROPIC ACTIVITY).
 CC -I- SIMILARITY: BELONGS TO THE KININ FAMILY.

KW Neuropeptide; Amidation.

FT MOD_RES 8
 SQ SEQUENCE 8 AA; 839 MW; 736365A5B9D6DD8 CRC64;

Query Match 24.7%; Score 22; DB 5; Length 8;
 Best Local Similarity 75.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NSWG 5
 DB 5 SSWG 8

RESULT 21

O77914 PRELIMINARY; PRT; 11 AA.

DT 01-NOV-1998 (TREMBLREL. 08, Created)

DT 01-NOV-1998 (TREMBLREL. 08, last sequence update)

DT 01-DEC-2001 (TREMBLREL. 19, last annotation update)

DE MHC class II B locus 9 (Fragment).

OS Oreochromis niloticus (Nile tilapia).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidel;

OC Cichlidae; Oreochromis.

NCBI_TaxID=8128;

RP SEQUENCE FROM N.A.
 RC MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RA "Linkage relationships and haplotype polymorphism among cichlid mhc
 RT class II B loci.";
 RL Genetics 149:1527-1537(1998).

DR EMBL: AF050025; AAC41364.1; -
FT NON_TER 1
SQ SEQUENCE 11 AA; 1167 MW; 2F46D347A2C045A3 CRC64;

Query Match
Best Local Similarity 24.7%; Score 22; DB 7; Length 11;
Matches 4; Conservative 3; Mismatches 1; Indels 4; Gaps 1;

OY 1 LNSMCKGRIIC 12
Db 1 MDSMS----IVC 8

RESULT 22

O56947 PRELIMINARY; PRT; 12 AA.

AC O56947;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE Hypothetical 1.6 kDa protein (Fragment).
OS Versinia pseudotuberculosis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX NCBI_TaxID=633;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GROUP IA;
RX MEDLINE=96125720; PubMed=8541300;
RA Hobbs M., Reeves P.R.;
RT "Genetic organization and evolution of Versinia pseudotuberculosis
RL Blochm. Biophys. Acta 1245:273-277(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=GROUP IA;
RX MEDLINE=97158136; PubMed=9004408;
RA Reeves P.R., Hobbs M., Valvano M.A., Skurnik M., Whitfield C.,
RT Coplin D., Kido N., Klena J., Maskell D., Raetz C.R., Rick P.D.;
RL Trends Microbiol. 4:495-503(1996).
DR EMBL: U29692; AAB48323.1; -
KW Hypothetical protein.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1563 MW; DB80264F3D433EB9 CRC64;

Query Match
Best Local Similarity 24.7%; Score 22; DB 2; Length 12;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 CKGRII 11
Db 6 CKNRYI 11

RESULT 23

O52920 PRELIMINARY; PRT; 13 AA.

AC O52920;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE Dctb and dcb genes, 5' end (Fragment).
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=387;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=90152354; PubMed=2695394;
RA Wang Y.-P., Birkenhead K., Boesten B., Manian S., O'Gara F.;
RT "Genetic analysis and regulation of the Rhizobium meliloti genes

RT controlling C-4-dicarboxylic acid transport."
RL Gene 85:135-144(1989).
DR EMBL: M33555; AAA26254.1; -
FT NON_TER 13
SQ SEQUENCE 13 AA; 1560 MW; D00F4BE521FEEBD CRC64;

Query Match
Best Local Similarity 24.7%; Score 22; DB 2; Length 13;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LNSMCK 6
Db 2 LPDMAC 7

RESULT 24

O9XLI2 PRELIMINARY; PRT; 13 AA.

AC O9XLI2;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE Cytochrome oxidase I (Fragment).
OS Bemisia tabaci (Sweetpotato whitefly).
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;
OC Aleyrodiformes; Aleyrodidae; Aleyrodinae; Bemisia.
OX NCBI_TaxID=7038;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=10583831;
RA Frohlich D.R., Torres-Jerez I., Bedford I.D., Markham P.G.,
RA Brown J.K.;
RT "A phylogeographical analysis of the Bemisia tabaci species complex
RT based on mitochondrial DNA markers."
RL Mol. Ecol. 8:1683-1691(1999).
DR EMBL: AF110703; AAD28415.1; -
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1639 MW; 8DD68729F5744365 CRC64;

Query Match
Best Local Similarity 24.7%; Score 22; DB 8; Length 13;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 NSMCK 6
Db 5 SSMYC 9

RESULT 25

O69142 PRELIMINARY; PRT; 15 AA.

AC O69142;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DE Protein SIC (Fragment).
GN SIC.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AP1;
RX MEDLINE=98298075; PubMed=9632622;
RA Berge A., Rasmussen M., Bjorck L.;
RT "Identification of an insertion sequence located in a region encoding
RL virulence factors of Streptococcus pyogenes."
DR EMBL: AF064540; AAC38769.1; -

DB 6 LSPWPC 11

RESULT 30

066202 PRELIMINARY; PRT; 12 AA.
 ID 066202: 072765;
 AC 066202: 072765;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Nucleocapsid protein (Fragment).
 OS Transmissible gastroenteritis virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
 OC Coronaviridae; Coronavirus.
 OX NCBI_TaxID=11149;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PURDUE-115;
 RX MEDLINE=87224815; PubMed=3035066;
 RA Laude H., Raschaert D., Huet J.C.;
 RT "Sequence and N-terminal processing of the transmembrane protein E1 of
 the coronavirus transmissible gastroenteritis virus.";
 RL J. Gen. Virol. 68:1687-1693(1987).
 DR EMBL; X05598; CAA29092.1; -
 KW Nucleocapsid.
 FT NON_TER
 SQ SEQUENCE 12 AA: 1348 MW: 35A1C53F9BD416D8 CRC64;

Query Match 23.6%; Score 21; DB 12; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4,7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 3 SWG 5
 Db 9 SWG 11

Search completed: June 5, 2003, 09:00:37
 Job time : 30 secs

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OM protein - protein search, using sw model

Run on: June 5, 2003, 08:58:39 ; Search time 34 Seconds
(without alignments)
58.787 Million cell updates/sec

Title: US-09-605-573a-69_COPY_12_26
Perfect score: 89
Sequence: 1 LNSWCCKGRICVTS 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 289567

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

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- 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
- 10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
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- 13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
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- 18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	96.6	16	19	AAW80468
2	86	96.6	17	19	AAW80474
3	81	91.0	16	19	AAW80467
4	77	86.5	16	21	AAV79852
5	77	86.5	20	21	AAV77396
6	75	84.3	16	21	AAV79848
7	75	84.3	16	21	AAV79851
8	74	83.1	16	21	AAV79846
9	72	80.9	15	17	AAW08268
10	72	80.9	15	17	AAW03053

11	72	80.9	15	17	AAW88790	HIV-1 subtype O gp
12	72	80.9	15	19	AAW64405	HIV epitope #8. S
13	72	80.9	15	19	AAW47240	HIV subtype O gp41
14	72	80.9	16	20	AAW82330	HIV-1 subtype O (A
15	72	80.9	16	21	AAV79845	HIV infection dete
16	72	80.9	16	21	AAV79845	HIV infection dete
17	72	80.9	16	21	AAV79847	HIV infection dete
18	72	80.9	16	21	AAV79858	HIV infection dete
19	70	78.7	16	21	AAV79854	HIV infection dete
20	70	78.7	16	21	AAV79857	HIV infection dete
21	69	77.5	16	21	AAV79841	HIV infection dete
22	69	77.5	16	21	AAV79850	HIV infection dete
23	69	77.5	20	18	AAW44580	Happen-peptide con
24	68	76.4	16	21	AAV79849	HIV infection dete
25	68	76.4	17	21	AAV67608	Peptide #8 for det
26	68	76.4	19	18	AAW44581	Happen-peptide con
27	68	76.4	19	18	AAW16381	HIV-1 sub-type B I
28	67	75.3	16	21	AAV79853	HIV infection dete
29	66	74.2	16	21	AAV79844	HIV infection dete
30	65	73.0	16	21	AAV79843	HIV infection dete
31	65	73.0	17	20	AAV05591	HIV-1 group O stra
32	64	71.9	16	21	AAV79856	HIV infection dete
33	64	71.9	17	21	AAV79828	HIV infection dete
34	64	71.9	17	21	AAV67618	Peptide #18 for de
35	63	70.8	16	21	AAV79855	HIV infection dete
36	63	70.8	19	18	AAW16380	HIV-1 sub-type B I
37	62	69.7	18	21	AAV79867	Putative HIV Immun
38	60	67.4	17	21	AAV79829	HIV infection dete
39	59	66.3	19	18	AAW16379	HIV-1 sub-type B I
40	58	65.2	10	20	AAV05593	HIV-1 group O stra
41	58	65.2	18	13	AAW82196	Sequence of synthe
42	58	65.2	19	11	AAW06326	Biologically determ
43	57	64.0	19	16	AAW94578	Synthetic HIV-2 en
44	57	64.0	19	17	AAW04219	HIV-2 gp36 Immunod
45	57	64.0	20	18	AAW35484	HIV peptide from H
46	56	62.9	12	20	AAV05598	HIV-1 group O stra
47	56	62.9	15	20	AAV05592	HIV-1 group O stra
48	56	62.9	17	11	AAW06056	Immunoreactive pep
49	55	61.8	16	19	AAW47242	HIV-1 gp41 derived
50	55	61.8	16	20	AAW82328	HIV-1 subtype F gp
51	55	61.8	16	20	AAW82329	HIV-1 subtype G gp
52	55	61.8	16	23	AAW67500	HIV-1 gp41 antigen
53	55	61.8	17	11	AAW06049	Immunoreactive pep
54	55	61.8	17	11	AAW06057	Immunoreactive pep
55	55	61.8	17	11	AAW06073	Immunoreactive pep
56	55	61.8	17	16	AAV76722	gp-41 epitope from
57	55	61.8	19	17	AAW03335	HIV-1 gp41/2 epit
58	54	60.7	11	20	AAV05594	HIV-1 gp41 group O
59	54	60.7	14	16	AAV76726	gp32 epitope from
60	54	60.7	14	19	AAW47241	HIV-2 gp33 derive
61	54	60.7	14	21	AAV79820	HIV infection dete
62	54	60.7	14	23	AAW76498	HIV-2 gp36 protein
63	54	60.7	15	17	AAW09341	Cyclic HIV principl
64	54	60.7	16	20	AAW82323	HIV-1 subtype A gp
65	54	60.7	16	20	AAW82324	HIV-1 subtype B gp
66	54	60.7	16	20	AAW82325	HIV-1 subtype C gp
67	54	60.7	17	11	AAW06048	Immunoreactive pep
68	54	60.7	17	11	AAW06071	Immunoreactive pep
69	54	60.7	17	11	AAW06072	Immunoreactive pep
70	54	60.7	17	11	AAW06089	Immunoreactive pep
71	54	60.7	17	17	AAW03340	HIV-2 gp32 epitope
72	54	60.7	18	11	AAW07508	Biologically determ
73	54	60.7	18	23	AAW76499	HIV-2 gp36 protein
74	54	60.7	19	11	AAW05143	Peptide epitopic f
75	54	60.7	19	18	AAW44677	Happen-peptide con
76	54	60.7	19	18	AAW16382	HIV-1 sub-type B I
77	54	60.7	20	11	AAW05156	Fusion protein epi
78	54	60.7	20	17	AAW04232	HIV-1 gp41 immunod
79	53	59.6	12	14	AAW41062	HIV-1 gp41 peptide
80	53	59.6	12	17	AAW81557	Mutation #1 of HIV
81	53	59.6	12	17	AAW93063	Mutation #1 of HIV
82	53	59.6	14	11	AAW03967	HIV-antibody react
83	53	59.6	15	9	AAW80178	Sequence of formul

84	53	59.6	15	9	AAp80217	Sequence of critic
85	53	59.6	15	20	AAy10339	T cell epitope/MHC
86	53	59.6	16	19	AAW85229	Helper T-cell pept
87	53	59.6	16	20	AAW82343	HIV-1 subtype D 9p
88	53	59.6	16	20	AAW82340	HIV-1 subtype D 9p
89	53	59.6	17	9	AAp80183	Sequence of formil
90	53	59.6	17	9	AAp81354	Sequence of critic
91	53	59.6	17	11	AAW80606	Immunoreactive pep
92	53	59.6	17	11	AAW80605	Immunoreactive pep
93	53	59.6	17	11	AAW80605	Immunoreactive pep
94	53	59.6	17	11	AAW80603	Immunoreactive pep
95	53	59.6	17	11	AAW80604	Immunoreactive pep
96	53	59.6	17	11	AAW80605	Immunoreactive pep
97	53	59.6	17	11	AAW80607	Immunoreactive pep
98	53	59.6	18	12	AAW14442	Biotin-tagged synt
99	53	59.6	19	9	AAp80179	Sequence of formil
100	53	59.6	19	9	AAp80218	Sequence of critic

ALIGNMENTS

RESULT 1

AAW80468
ID AAW80468 standard; peptide; 16 AA.

XX
AC AAW80468;

XX
DT 28-JAN-1999 (first entry)

XX
DE Peptide derived from a conserved sequence of group O human HIV.

XX
KM Group O human immune deficiency virus; HIV; detection; infection.

XX
OS Synthetic.

OS
OS Immune deficiency virus.

XX
PN W09845323-A1.

XX
PD 15-OCT-1998.

XX
PF 06-APR-1998; 98W0-FR00691.

XX
PR 24-FEB-1998; 98FR-0002212.

XX
PR 09-APR-1997; 97FR-0004356.

XX
PA (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.

XX
PI Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;

XX
DR WPI; 1998-583190/49.

XX
PT New synthetic peptide(s) - useful for, e.g. detecting infection by

XX
PT human immune deficiency virus of group O

XX
PS Claim 6; Page 43; 55pp; French.

XX
CC AAW80459-74 represent synthetic peptides (either linear or cyclised by

XX
CC Cys-Cys disulphide bonds). The peptides represent variable sequences

XX
CC connected around short highly conserved sequences present in isolates

XX
CC of group O human immune deficiency virus (HIV). The peptides are

XX
CC useful as immunological reagents for detecting infection by group O

XX
CC human immune deficiency virus (HIV).

XX
SQ Sequence 16 AA;

Query Match 96.6%; Score 86; DB 19; Length 16;

Best Local Similarity 86.7%; Pred. No. 2.4e-06;

Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNSWGCKGRIVCYTS 15
DB 2 LNSWGCKGRIVCYTS 16

RESULT 2

AAW80474
ID AAW80474 standard; peptide; 17 AA.

XX
AC AAW80474;

XX
DT 28-JAN-1999 (first entry)

XX
DE Peptide derived from a conserved sequence of group O human HIV.

XX
KM Group O human immune deficiency virus; HIV; detection; infection.

XX
OS Synthetic.

OS
OS Immune deficiency virus.

XX
PN W09845323-A1.

XX
PD 15-OCT-1998.

XX
PF 06-APR-1998; 98W0-FR00691.

XX
PR 24-FEB-1998; 98FR-0002212.

XX
PR 09-APR-1997; 97FR-0004356.

XX
PA (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.

XX
PI Cheneboux DMB, Delagneau JFH, Gabelle SJX, Rieunier FY;

XX
DR WPI; 1998-583190/49.

XX
PT New synthetic peptide(s) - useful for, e.g. detecting infection by

XX
PT human immune deficiency virus of group O

XX
PS Claim 6; Page 45; 55pp; French.

XX
CC AAW80459-74 represent synthetic peptides (either linear or cyclised by

XX
CC Cys-Cys disulphide bonds). The peptides represent variable sequences

XX
CC connected around short highly conserved sequences present in isolates

XX
CC of group O human immune deficiency virus (HIV). The peptides are

XX
CC useful as immunological reagents for detecting infection by group O

XX
CC human immune deficiency virus (HIV).

XX
SQ Sequence 17 AA;

Query Match 96.6%; Score 86; DB 19; Length 17;

Best Local Similarity 86.7%; Pred. No. 2.6e-06;

Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNSWGCKGRIVCYTS 15
DB 2 LNSWGCKGRIVCYTS 16

XX
DT 28-JAN-1999 (first entry)

XX
DE Peptide derived from a conserved sequence of group O human HIV.

XX
KM Group O human immune deficiency virus; HIV; detection; infection.

XX
OS Synthetic.

OS
OS Immune deficiency virus.

XX
PN W09845323-A1.

XX
PD 15-OCT-1998.

XX 06-APR-1998; 98WO-FR00691.
PF
XX 24-FEB-1998; 98FR-0002212.
PR 09-APR-1997; 97FR-0004356.
XX
PA (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.
XX
PI Cheneboux DMB, Delagneau JFH, Gadelle SJX, Rieunier FY;
XX WPI: 1998-583190/49.
DR
XX New synthetic peptide(s) - useful for, e.g., detecting infection by
PT human immune deficiency virus of group O
XX
XX Claim 6; Page 43; 55pp; French.
PS
XX AAM80459-74 represent synthetic peptides (either linear or cyclised by
CC Cys-Cys disulphide bonds). The peptides represent variable sequences
CC connected around short highly conserved sequences present in isolates
CC of group O human immune deficiency virus (HIV). The peptides are
CC useful as immunological reagents for detecting infection by group O
CC human immune deficiency virus (HIV).
CC
SQ Sequence 16 AA:

Query Match 91.0%; Score 81; DB 19; Length 16;
Best Local Similarity 80.0%; Pred. No. 1.4e-05;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNSMGCKGRICVTS 15
I:|||||I::|||
Db 2 LSSMGCKGRICVTS 16

RESULT 4
AAV79852
ID AAV79852 standard; Peptide; 16 AA.
XX
AC AAV79852;
XX
DT 10-MAY-2000 (first entry)
XX
DE HIV infection detection peptide SEQ ID NO:90.
XX
KW Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;
KW viral chimeric peptide; therapy; immunological.
XX
OS Unidentified.
XX
PN WO200001719-A2.
XX
PD 13-JAN-2000.
XX
PF 02-JUL-1999; 99WO-US15114.
XX
PR 02-JUL-1998; 98US-0091659.
PR 16-OCT-1998; 98US-0104685.
PR 11-DEC-1998; 98US-0112026.
XX
PA (PEPT-) PEPTIDE SOLUTIONS.
XX
PI Chowdhury AM, Bernstein D, Kozhich A, Motsenbocker M;
XX WPI: 2000-171000/15.
DR
XX Novel viral-derived peptides used for the detection of human
PT immunodeficiency virus (HIV) infection, particularly HIV-2 infection
XX
PS Disclosure; Fig 1; 67pp; English.
CC The present invention describes a peptide (I) for detecting HIV-2
CC infection, which comprises a core Varicella-zoster protein 51 sequence.

CC also described in the present invention are methods for detecting HIV
CC infection. Peptides from the present invention can be used for the
CC immunological detection of anti-HIV antibody, particularly for HIV-2
CC testing. The peptides have high sensitivity and selectivity for HIV.
CC The improved peptides have increased stability which allows the
CC peptides to react more favourably to give more sensitive tests. AAV79763
CC to AAV7968 represent peptides used in the exemplification of the
CC present invention.
CC
SQ Sequence 16 AA:

Query Match 86.5%; Score 77; DB 21; Length 16;
Best Local Similarity 73.3%; Pred. No. 5.4e-05;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNSMGCKGRICVTS 15
I|||||I::|||
Db 1 LNSMGCKGRICVTS 15

RESULT 5
AAV7396
ID AAV7396 standard; peptide; 20 AA.
XX
AC AAV7396;
XX
DT 22-MAY-2000 (first entry)
XX
DE HIV-1 group O env epitope, SEQ ID NO:112.
XX
KW HIV-1 group O; env; gp120; gp41; glycoprotein; monoclonal antibody;
KW immunosay; positive control; affinity purification; therapeutic;
KW Escherichia coli; reactive; epitope.
XX
OS Human immunodeficiency virus type 1 group O.
OS Synthetic.
XX
PN WO200004383-A2.
XX
PD 27-JAN-2000.
XX
PF 09-JUL-1999; 99WO-US15469.
XX
PR 14-JUL-1998; 98US-0115171.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Scheffel JW, Hackett JR, Tyner JD, Hickman RK;
XX WPI: 2000-171290/15.
DR
XX Novel monoclonal antibodies useful as positive control reagent for
PT detecting human immunodeficiency virus infections and diagnosing,
PT evaluating or prognosing viral disease
XX
PS Claim 20; Page 70; 148pp; English.
XX
XX The invention relates to anti-HIV-1 group O monoclonal antibodies, which
CC may be used as positive control reagents in immunoassays to detect and
CC differentiate HIV-1 infections. The invention also encompasses a
CC monoclonal antibody which binds specifically to an HIV-1 group O
CC antigen, which has no more than 15% cross reactivity to a corresponding
CC antigen selected from HIV-1 group M antigens and HIV-2 antigens; and a
CC method of using a monoclonal antibody as a positive control reagent in
CC an immunoassay for the detection of anti HIV-1 group O antibodies. The
CC monoclonal antibodies are useful as positive control reagents in
CC immunoassays capable of detecting anti-HIV-1 group O antibodies. Such
CC immunoassays involve coupling a monoclonal antibody with HIV group-1
CC antigen and detecting the antigen-antibody complex. The monoclonal
CC antibodies of the invention would be used to ensure that the reagents
CC provided to detect HIV-1 group O antibody were performing properly. The
CC monoclonal antibodies may also can be immobilised on a matrix and used
CC for affinity purification of specific HIV-1 group O-derived proteins

CC from cell cultures or biological tissues. The monoclonal antibodies can
CC also be used for generating chimeric antibodies for therapeutic use.
CC different synthetic, recombinant or purified antibodies which identify
CC different epitopes of HIV antigens can be used in combination in assay to
CC diagnose, evaluate, or prognosticate HIV disease condition. The
CC monoclonal antibodies are also useful for differentiating HIV-1 Group O
CC antigens from HIV-group M and HIV-2 antigens. Sequences AAY77389-Y77398
CC represent HIV-1 group O env epitopes.

XX
SQ Sequence 20 AA;

Query Match 86.5%; Score 77; DB 21; Length 20;

Best Local Similarity 85.7%; Pred. No. 6.7e-05; Mismatches 1; Indels 0; Gaps 0;

Matches 12; Conservative 1; Indels 0; Gaps 0;
OY 1 LNSMGCKGRICVT 14
Db 7 LNSMGCKGRICVT 20

RESULT 6

AA79848
ID AAY79848 standard; Peptide; 16 AA.

XX
AC AAY79848;

XX
DT 10-MAY-2000 (first entry)

XX
DE HIV infection detection peptide SEQ ID NO:86.

XX
KW Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;

XX
KM viral chimeric peptide; therapy; immunological.

XX
OS Unidentified.

XX
PN WO200001719-A2.

XX
PD 13-JAN-2000.

XX
PF 02-JUL-1999; 99WO-US15114.

XX
PR 02-JUL-1998; 98US-0091659.

XX
PR 16-OCT-1998; 98US-0104685.

XX
PR 11-DEC-1998; 98US-0112026.

XX
PA (PEPT-) PEPTIDE SOLUTIONS.

XX
PI Chowdhury AM, Bernstein D, Kozhich A, Molsenbocker M;

XX
DR WPI; 2000-171000/15.

XX
PT Novel viral-derived peptides used for the detection of human

XX
PS immunodeficiency virus (HIV) infection, particularly HIV-2 infection

XX
PS Disclosure; Fig 1; 67pp; English.

CC The present invention describes a peptide (I) for detecting HIV-2
CC infection, which comprises a core Varicella-Zoster protein 51 sequence.
CC also described in the present invention are methods for detecting HIV
CC infection. Peptides from the present invention can be used for the
CC immunological detection of anti-HIV antibody, particularly for HIV-2
CC testing. The peptides have high sensitivity and selectivity for HIV.
CC The improved peptides have increased stability which allows the
CC peptides to react more favourably to give more sensitive tests. AAY79763
CC to AAY79868 represent peptides used in the exemplification of the
CC present invention.

XX
SQ Sequence 16 AA;

Query Match 84.3%; Score 75; DB 21; Length 16;

Best Local Similarity 80.0%; Pred. No. 0.00011; Mismatches 2; Indels 0; Gaps 0;

OY 1 LNSMGCKGRICVT 15
Db 1 LNSMGCKGRICVT 15

RESULT 7

AA79851
ID AAY79851 standard; Peptide; 16 AA.

XX
AC AAY79851;

XX
DT 10-MAY-2000 (first entry)

XX
DE HIV infection detection peptide SEQ ID NO:89.

XX
KW Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;

XX
KM viral chimeric peptide; therapy; immunological.

XX
OS Unidentified.

XX
PN WO200001719-A2.

XX
PD 13-JAN-2000.

XX
PF 02-JUL-1999; 99WO-US15114.

XX
PR 02-JUL-1998; 98US-0091659.

XX
PR 16-OCT-1998; 98US-0104685.

XX
PR 11-DEC-1998; 98US-0112026.

XX
PA (PEPT-) PEPTIDE SOLUTIONS.

XX
PI Chowdhury AM, Bernstein D, Kozhich A, Molsenbocker M;

XX
DR WPI; 2000-171000/15.

XX
PT Novel viral-derived peptides used for the detection of human

XX
PS immunodeficiency virus (HIV) infection, particularly HIV-2 infection

XX
PS Disclosure; Fig 1; 67pp; English.

CC The present invention describes a peptide (I) for detecting HIV-2
CC infection, which comprises a core Varicella-Zoster protein 51 sequence.
CC also described in the present invention are methods for detecting HIV
CC infection. Peptides from the present invention can be used for the
CC immunological detection of anti-HIV antibody, particularly for HIV-2
CC testing. The peptides have high sensitivity and selectivity for HIV.
CC The improved peptides have increased stability which allows the
CC peptides to react more favourably to give more sensitive tests. AAY79763
CC to AAY79868 represent peptides used in the exemplification of the
CC present invention.

XX
SQ Sequence 16 AA;

Query Match 84.3%; Score 75; DB 21; Length 16;

Best Local Similarity 80.0%; Pred. No. 0.00011; Mismatches 2; Indels 0; Gaps 0;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 LNSMGCKGRICVT 15
Db 1 LNSMGCKGRICVT 15

RESULT 8

AA79846
ID AAY79846 standard; Peptide; 16 AA.

XX
AC AAY79846;

XX
DT 10-MAY-2000 (first entry)

XX
DE HIV infection detection peptide SEQ ID NO:84.

XX

PS Claims 14, 21; Pages 21, 22; 23pp; German.

XX New hapten-labelled peptides are claimed which consist of (1) a
 CC peptide of max. length 50 amino acids, and (2) a hapten attached
 CC to the peptide at the N-terminal or at a side chain amino group. The
 CC hapten is a steroid, bile acid, sex hormone, corticoid, cardenolide (or
 CC its glycoside), bufadienolide, steroid-sapogenin or a steroid alkaloid.
 CC The labelled peptides are useful for immunological determination of
 CC antibodies against bacteria, viruses, protozoa or autoimmune
 CC antigens, etc., esp. antibodies against HIV or hepatitis C virus. The
 CC peptide consists of an immunologically reactive epitope region and a
 CC spacer region (of 1-10 amino acids which contain charged groups or
 CC groups able to form H-bonds). The present sequence represents a
 CC preferred epitope region which can be used in the labelled peptides.

SO Sequence 15 AA;

Query Match 80.9%; Score 72; DB 17; Length 15;
 Best Local Similarity 66.7%; Pred. No. 0.00029;
 Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 LNSWGCKGRICVYTS 15
 1 LSLWGCKRLVCTYS 15

Db 1 LSLWGCKRLVCTYS 15

RESULT 11
 AAR88790
 ID AAR88790 standard; peptide; 15 AA.

XX AAR88790;
 AC
 XX 01-OCT-1996 (first entry)
 DT
 XX HIV-1 subtype O gp41 epitope labelled by metal chelate.
 DE
 XX HIV-1; HIV-1; glycoprotein gp41; epitope; antigen; immunoassay;
 KM metal chelate-labelled.
 XX
 XX Human immunodeficiency virus type 1.
 OS
 XX
 XX Key Location/Qualifiers
 PH Modified-site 1..15
 FT /note= "at least one of N-terminus and/or side-chain
 FT amino groups is modified post-synthesis by
 FT coupling of an activated luminescent metal
 FT chelate (LMC) or at least one amino acid
 FT covalently coupled to a LMC is incorporated
 FT during peptide synthesis"

XX DE4430998-A1.
 PN
 XX 01-FEB-1996.
 PD
 XX 31-AUG-1994; 94DE-4430998.
 PF
 XX 25-JUL-1994; 94DE-4426276.
 PR
 XX (BOEF) BOEHRINGER MANNHEIM GMBH.
 PA
 XX Seidel C, Hoess E, Wienhues-Thelen U;
 PI
 XX WPI: 1996-130246/14.
 DR
 XX Prepn. of metal chelate labelled peptide(s) for use as antigens
 PT in immunoassays of antibodies, by reacting activated chelate with
 PT prim. amino gps. in a peptide, also new chelate-contg. amino acids
 PT
 XX Claim 23; Page 19; 21pp; German.

PS New metal chelate-labelled peptides are claimed which consist of (1)
 CC a peptide of max. length 50 amino acids, and (2) a luminescent
 CC metal chelate attached to the peptide at the N-terminal or at a side-

CC chain amino group. The chelates pref. contain Re, Ir, Os or esp. Ru
 CC and the ligands are aromatic, heterocyclic polydentate ligands such
 CC as bipyridyl, bipyrazyl, terpyridyl or phenanthrolyl.
 CC The labelled peptides are useful for immunological determination of
 CC antibodies against bacteria, viruses, protozoa or autoimmune
 CC antigens, etc., esp. antibodies against HIV or hepatitis C virus. The
 CC peptide consists of an immunologically reactive epitope region and a
 CC spacer region (of 1-10 amino acids which contain charged groups or
 CC groups able to form H-bonds). The present sequence represents a
 CC preferred epitope region from HIV-1 subtype O which can be used in
 CC the labelled peptides.

SO Sequence 15 AA;

Query Match 80.9%; Score 72; DB 17; Length 15;
 Best Local Similarity 66.7%; Pred. No. 0.00029;
 Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 LNSWGCKGRICVYTS 15
 1 LSLWGCKRLVCTYS 15

Db 1 LSLWGCKRLVCTYS 15

RESULT 12
 AAW64405
 ID AAW64405 standard; peptide; 15 AA.

XX AAW64405;
 AC
 XX 08-OCT-1998 (first entry)
 DT
 XX HIV epitope #8.
 DE
 XX Epitope; solid phase synthesis; end capping; immunoassay; HIV; antibody;
 KM human immunodeficiency virus; sandwich assay.
 XX
 XX Synthetic.
 OS Human immunodeficiency virus.
 XX
 XX DE19654764-A1.
 PN
 XX 02-JUL-1998.
 PD
 XX 30-DEC-1996; 96DE-1054764.
 PF
 XX 30-DEC-1996; 96DE-1054764.
 PR
 XX (BOEF) BOEHRINGER MANNHEIM GMBH.
 PA
 XX Paatz E, Hoess E, Ofenloch-Haehnle B;
 PI
 XX WPI: 1998-363726/32.
 DR
 XX Production of peptide libraries - by solid-phase synthesis with
 PT end-capping of incomplete sequences
 PT
 XX Claim 12; Page 4; 14pp; German.

PS AAW64398-W64407 are peptide epitopes used in a novel method for
 CC producing a peptide mixture from amino acid derivatives on a solid phase
 CC and then cleaving the peptides from the solid phase. A mixture of
 CC derivatives of different amino acids is used for the coupling reaction
 CC in at least 1 amino acid position. After each coupling step in which a
 CC mixture of derivatives of different amino acids is used, peptide
 CC sequences to which no amino acid was coupled in that step are
 CC selectively end-capped. The peptides are used in immunoassays for
 CC antibodies, preferably sandwich assays, especially for HIV subtype
 CC determination. End-capping prevents the generation of peptide sequences
 CC that are only slightly shorter than the full length, thereby
 CC facilitating purification of the full-length peptides.

SO Sequence 15 AA;

XX 02-JUL-1998; 98US-0091659.
PR 16-OCT-1998; 98US-0104685.
PR 11-DEC-1998; 98US-0112026.
XX (PEPT-) PEPTIDE SOLUTIONS.
XX Chowdhury AM, Bernstein D, Kozhich A, Molsenbocker M;
XX WPI; 2000-171000/15.
XX
XX Novel viral-derived peptides used for the detection of human
XX immunodeficiency virus (HIV) infection, particularly HIV-2 infection
XX disclosure; Fig 1; 67pp; English.
XX
XX The present invention describes a peptide (1) for detecting HIV-2
XX infection, which comprises a core Varicella-zoster protein 51 sequence.
XX also described in the present invention are methods for detecting HIV
XX infection. Peptides from the present invention can be used for the
XX immunological detection of anti-HIV antibody, particularly for HIV-2
XX testing. The peptides have high sensitivity and selectivity for HIV.
XX The improved peptides have increased stability which allows the
XX peptides to react more favourably to give more sensitive tests. AAY79763
XX to AAY79868 represent peptides used in the exemplification of the
XX present invention.
XX
XX Sequence 16 AA;
XX
XX Query Match 80.9%; Score 72; DB 21; Length 16;
XX Best Local Similarity 73.3%; Pred. No. 0.00031;
XX Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 LNSWCKGRRLICYTS 15
XX 1 LNWGCGARKVCYTS 15
XX
XX Db
XX
XX RESULT 16
XX AAY79845
XX ID AAY79845 standard; Peptide; 16 AA.
XX
XX AAY79845;
XX
XX 10-MAY-2000 (first entry)
XX
XX HIV infection detection peptide SEQ ID NO:83.
XX
XX Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;
XX viral chimeric peptide; therapy; immunological.
XX
XX Unidentified.
XX
XX WO200001719-A2.
XX
XX 13-JAN-2000.
XX
XX 02-JUL-1999; 99WO-US15114.
XX
XX 02-JUL-1998; 98US-0091659.
XX 16-OCT-1998; 98US-0104685.
XX 11-DEC-1998; 98US-0112026.
XX
XX (PEPT-) PEPTIDE SOLUTIONS.
XX
XX Chowdhury AM, Bernstein D, Kozhich A, Molsenbocker M;
XX WPI; 2000-171000/15.
XX
XX Novel viral-derived peptides used for the detection of human
XX immunodeficiency virus (HIV) infection, particularly HIV-2 infection
XX disclosure; Fig 1; 67pp; English.

XX The present invention describes a peptide (1) for detecting HIV-2
XX infection, which comprises a core Varicella-zoster protein 51 sequence.
XX also described in the present invention are methods for detecting HIV
XX infection. Peptides from the present invention can be used for the
XX immunological detection of anti-HIV antibody, particularly for HIV-2
XX testing. The peptides have high sensitivity and selectivity for HIV.
XX The improved peptides have increased stability which allows the
XX peptides to react more favourably to give more sensitive tests. AAY79763
XX to AAY79868 represent peptides used in the exemplification of the
XX present invention.
XX
XX Sequence 16 AA;
XX
XX Query Match 80.9%; Score 72; DB 21; Length 16;
XX Best Local Similarity 73.3%; Pred. No. 0.00031;
XX Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 LNSWCKGRRLICYTS 15
XX 1 LNWGCGARKVCYTS 15
XX
XX Db
XX
XX RESULT 17
XX AAY79847
XX ID AAY79847 standard; Peptide; 16 AA.
XX
XX AAY79847;
XX
XX 10-MAY-2000 (first entry)
XX
XX HIV infection detection peptide SEQ ID NO:85.
XX
XX Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;
XX viral chimeric peptide; therapy; immunological.
XX
XX Unidentified.
XX
XX WO200001719-A2.
XX
XX 13-JAN-2000.
XX
XX 02-JUL-1999; 99WO-US15114.
XX
XX 02-JUL-1998; 98US-0091659.
XX 16-OCT-1998; 98US-0104685.
XX 11-DEC-1998; 98US-0112026.
XX
XX (PEPT-) PEPTIDE SOLUTIONS.
XX
XX Chowdhury AM, Bernstein D, Kozhich A, Molsenbocker M;
XX WPI; 2000-171000/15.
XX
XX Novel viral-derived peptides used for the detection of human
XX immunodeficiency virus (HIV) infection, particularly HIV-2 infection
XX disclosure; Fig 1; 67pp; English.
XX
XX The present invention describes a peptide (1) for detecting HIV-2
XX infection, which comprises a core Varicella-zoster protein 51 sequence.
XX also described in the present invention are methods for detecting HIV
XX infection. Peptides from the present invention can be used for the
XX immunological detection of anti-HIV antibody, particularly for HIV-2
XX testing. The peptides have high sensitivity and selectivity for HIV.
XX The improved peptides have increased stability which allows the
XX peptides to react more favourably to give more sensitive tests. AAY79763
XX to AAY79868 represent peptides used in the exemplification of the
XX present invention.
XX
XX Sequence 16 AA;
XX
XX Query Match 80.9%; Score 72; DB 21; Length 16;

Best Local Similarity 73.3%; Pred. No. 0.00031;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 LNSMGCKGRICVTS 15
DB 1 LNSMGCKGRICVTS 15

RESULT 18

AAV79858
ID AAV79858 standard; Peptide: 16 AA.

AC AAV79858;

DT 10-MAY-2000 (first entry)

DE HIV infection detection peptide SEQ ID NO:96.

KM Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;
XX viral chimeric peptide; therapy; immunological.

OS Unidentified.

PN WO200001719-A2.

PD 13-JAN-2000.

PF 02-JUL-1999; 99WO-US15114.

PR 02-JUL-1998; 98US-0091659.

PR 16-OCT-1998; 98US-0104685.

PR 11-DEC-1998; 98US-0112026.

PA (PEPT-) PEPTIDE SOLUTIONS.

PI Chowdhury AM, Bernstein D, Kozhich A, Molsenbocker M;

DR WPI: 2000-171000/15.

PT Novel viral-derived peptides used for the detection of human
XX immunodeficiency virus (HIV) infection, particularly HIV-2 infection

PS Disclosure; Fig 1; 67pp; English.

XX The present invention describes a peptide (1) for detecting HIV-2
CC infection, which comprises a core Varicella-zoster protein 51 sequence.
CC also described in the present invention are methods for detecting HIV
CC infection. Peptides from the present invention can be used for the
CC immunological detection of anti-HIV antibody, particularly for HIV-2
CC testing. The peptides have high sensitivity and selectivity for HIV-2
CC The improved peptides have increased stability which allows the
CC peptides to react more favourably to give more sensitive tests.
CC to AAV79868 represent peptides used in the exemplification of the
CC present invention. AAV79763

XX Sequence 16 AA;

Query Match 80.9%; Score 72; DB 21; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.00031;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 LNSMGCKGRICVTS 15
DB 1 LNSMGCKGRICVTS 15

RESULT 19

AAV79854
ID AAV79854 standard; Peptide: 16 AA.

AC AAV79854;

DT 10-MAY-2000 (first entry)

XX HIV infection detection peptide SEQ ID NO:92.
DE
XX
XX Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;
KM viral chimeric peptide; therapy; immunological.

XX Unidentified.

OS WO200001719-A2.

PN 13-JAN-2000.

PD 02-JUL-1999; 99WO-US15114.

PF 02-JUL-1998; 98US-0091659.

PR 16-OCT-1998; 98US-0104685.

PR 11-DEC-1998; 98US-0112026.

PA (PEPT-) PEPTIDE SOLUTIONS.

PI Chowdhury AM, Bernstein D, Kozhich A, Molsenbocker M;

DR WPI: 2000-171000/15.

PT Novel viral-derived peptides used for the detection of human
XX immunodeficiency virus (HIV) infection, particularly HIV-2 infection

PS Disclosure; Fig 1; 67pp; English.

XX The present invention describes a peptide (1) for detecting HIV-2
CC infection, which comprises a core Varicella-zoster protein 51 sequence.
CC also described in the present invention are methods for detecting HIV
CC infection. Peptides from the present invention can be used for the
CC immunological detection of anti-HIV antibody, particularly for HIV-2
CC testing. The peptides have high sensitivity and selectivity for HIV-2
CC The improved peptides have increased stability which allows the
CC peptides to react more favourably to give more sensitive tests.
CC to AAV79868 represent peptides used in the exemplification of the
CC present invention. AAV79763

XX Sequence 16 AA;

Query Match 78.7%; Score 70; DB 21; Length 16;
Best Local Similarity 73.3%; Pred. No. 0.00061;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 LNSMGCKGRICVTS 15
DB 1 LNSMGCKGRICVTS 15

RESULT 20

AAV79857
ID AAV79857 standard; Peptide: 16 AA.

AC AAV79857;

DT 10-MAY-2000 (first entry)

DE HIV infection detection peptide SEQ ID NO:95.

KM Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;
XX viral chimeric peptide; therapy; immunological.

OS Unidentified.

PN WO200001719-A2.

PD 13-JAN-2000.

PF 02-JUL-1999; 99WO-US15114.

PR 02-JUL-1998; 98US-0091659.

PR 16-OCT-1998; 98US-0104685.
PR 11-DEC-1998; 98US-0112026.
XX
XX (PEPT-) PEPTIDE SOLUTIONS.
XX Chowdhury AM, Bernstein D, Kozhich A, Molsenbocker M;
XX WPI; 2000-171000/15.
XX
XX Novel viral-derived peptides used for the detection of human
XX immunodeficiency virus (HIV) infection, particularly HIV-2 infection
XX
XX Disclosure; Fig 1; 67pp; English.
XX
XX The present invention describes a peptide (I) for detecting HIV-2
XX infection, which comprises a core Varicella-zoster protein 51 sequence.
XX also described in the present invention are methods for detecting HIV
XX infection. Peptides from the present invention can be used for the
XX immunological detection of anti-HIV antibody, particularly for HIV-2
XX testing. The peptides have high sensitivity and selectivity for HIV.
XX The improved peptides have increased stability which allows the
XX peptides to react more favourably to give more sensitive tests. AAY79763
XX to AAY79868 represent peptides used in the exemplification of the
XX present invention.
XX
XX Sequence 16 AA;
XX
XX Query Match 78.7%; Score 70; DB 21; Length 16;
XX Best Local Similarity 73.3%; Pred. No. 0.00061;
XX Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 1 LNSWCGKGRICVTS 15
DB 1 LNPWGCAKQVCYTS 15

RESULT 21
AAY79841
ID AAY79841 standard; Peptide: 16 AA.
XX
XX AAY79841;
XX 10-MAY-2000 (first entry)
XX
XX HIV infection detection peptide SEQ ID NO:79.
XX
XX Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;
XX viral chimeric peptide; therapy; immunological.
XX
XX Unidentified.
XX
XX OS
XX
XX W0200001719-A2.
XX
XX 13-JAN-2000.
XX
XX 02-JUL-1999; 99WO-US15114.
XX
XX 02-JUL-1998; 98US-0091659.
XX 16-OCT-1998; 98US-0104685.
XX 11-DEC-1998; 98US-0112026.
XX
XX (PEPT-) PEPTIDE SOLUTIONS.
XX
XX Chowdhury AM, Bernstein D, Kozhich A, Molsenbocker M;
XX WPI; 2000-171000/15.
XX
XX Novel viral-derived peptides used for the detection of human
XX immunodeficiency virus (HIV) infection, particularly HIV-2 infection
XX
XX Disclosure; Fig 1; 67pp; English.
XX
XX The present invention describes a peptide (I) for detecting HIV-2

CC infection, which comprises a core Varicella-zoster protein 51 sequence.
CC also described in the present invention are methods for detecting HIV
CC infection. Peptides from the present invention can be used for the
CC immunological detection of anti-HIV antibody, particularly for HIV-2
CC testing. The peptides have high sensitivity and selectivity for HIV.
CC The improved peptides have increased stability which allows the
CC peptides to react more favourably to give more sensitive tests. AAY79763
CC to AAY79868 represent peptides used in the exemplification of the
CC present invention.
CC
CC Sequence 16 AA;
CC
CC Query Match 77.5%; Score 69; DB 21; Length 16;
CC Best Local Similarity 66.7%; Pred. No. 0.00086;
CC Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
OY 1 LNSWCGKGRICVTS 15
DB 1 LNPWGCAKQVCYTS 15

RESULT 22
AAY79850
ID AAY79850 standard; Peptide: 16 AA.
XX
XX AAY79850;
XX 10-MAY-2000 (first entry)
XX
XX HIV infection detection peptide SEQ ID NO:88.
XX
XX Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;
XX viral chimeric peptide; therapy; immunological.
XX
XX Unidentified.
XX
XX OS
XX
XX W0200001719-A2.
XX
XX 13-JAN-2000.
XX
XX 02-JUL-1999; 99WO-US15114.
XX
XX 02-JUL-1998; 98US-0091659.
XX 16-OCT-1998; 98US-0104685.
XX 11-DEC-1998; 98US-0112026.
XX
XX (PEPT-) PEPTIDE SOLUTIONS.
XX
XX Chowdhury AM, Bernstein D, Kozhich A, Molsenbocker M;
XX WPI; 2000-171000/15.
XX
XX Novel viral-derived peptides used for the detection of human
XX immunodeficiency virus (HIV) infection, particularly HIV-2 infection
XX
XX Disclosure; Fig 1; 67pp; English.
XX
XX The present invention describes a peptide (I) for detecting HIV-2
XX infection, which comprises a core Varicella-zoster protein 51 sequence.
XX also described in the present invention are methods for detecting HIV
XX infection. Peptides from the present invention can be used for the
XX immunological detection of anti-HIV antibody, particularly for HIV-2
XX testing. The peptides have high sensitivity and selectivity for HIV.
XX The improved peptides have increased stability which allows the
XX peptides to react more favourably to give more sensitive tests. AAY79763
XX to AAY79868 represent peptides used in the exemplification of the
XX present invention.
XX
XX Sequence 16 AA;
XX
XX Query Match 77.5%; Score 69; DB 21; Length 16;
XX Best Local Similarity 73.3%; Pred. No. 0.00086;
XX Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 LNSWCKGRICYS 15
 ||||| | : |||||
 Db 1 LNSWCKANROVCYTS 15

RESULT 23

AAW44680 standard; peptide: 20 AA.

AAW44680;

01-MAY-1998 (first entry)

Hapten-peptide conjugate #4 to detect anti-HIV-1 antibodies.

Hapten-peptide: HIV; immunoassay; detection; antibody; HIV-1;

capture reagent; haptenised peptide; HIV-2.

Synthetic.

Human immunodeficiency virus type 1.

Modified-site.

Location/Qualifiers

1 /note- "Alpha amino group of Lys1 is optionally modified by biotin-aminocaproyl"

MO9641187-A1.

19-DEC-1996.

07-JUN-1996; 96WO-US09507.

07-JUN-1995; 95US-0486657.

(ABBO) ABBOTT LAB.

Bridon DP, Chang C, Colpitts TL, Dagfal DJ, Jaffe K;

Merchant BR, Sze I;

WPI; 1997-108656/10.

Immunosay for HIV specific antibody detection - uses peptide

haptenised at N terminus for reaction with the initial complex of

antibody and capture reagent

Claim 1; Page 8; 37pp; English.

This sequence represents a peptide derived from the human immuno-

deficiency virus-1 (HIV-1) gp41, type 0. N-terminal haptenised peptides

or -2 antibodies (Ab). The method comprises: (1) reacting sample with

capture reagent (CR) to form a CR-Ab complex (C); (11) treating this

complex with a haptenised peptide conjugate (Cj) to form a C-Cj complex;

(111) detecting this with an indicator (I) to form a C-Cj-I complex; and

(1iv) detecting a signal generated from I. The hapten is attached at a

known, predetermined position, outside the epitope so that it cannot

interfere with binding to antibody. This provides a better assay than

similar peptides haptenised randomly in solution.

Sequence 20 AA:

Query Match 77.5%; Score 69; DB 18; Length 20;

Best Local Similarity 71.4%; Pred. NO. 0.0011;

Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LNSWCKGRICYT 14

1 : ||||| : |||||

Db 7 LSIWCKGKRLICYT 20

1 : ||||| : |||||

RESULT 24

AAV79849

ID AAV79849 standard; peptide: 16 AA.

AAV79849;

10-MAY-2000 (first entry)

HIV infection detection peptide SEQ ID NO:87.

Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;

viral chimeric peptide; therapy; immunological.

Unidentified.

MO200001719-A2.

13-JAN-2000.

02-JUL-1999; 99WO-US15114.

02-JUL-1998; 98US-0091659.

16-OCT-1998; 98US-0104685.

11-DEC-1998; 98US-0112026.

(PEPT-) PEPTIDE SOLUTIONS.

Chowdhury AM, Bernstein D, Kozhich A, Molsenbocker M;

WPI; 2000-171000/15.

Novel viral-derived peptides used for the detection of human

immunodeficiency virus (HIV) infection, particularly HIV-2 infection

Disclosure; Fig 1; 67pp; English.

The present invention describes a peptide (I) for detecting HIV-2

infection, which comprises a core varicella-zoster protein 51 sequence.

also described in the present invention are methods for detecting HIV

infection. Peptides from the present invention can be used for the

immunological detection of anti-HIV antibody, particularly for HIV-2

testing. The peptides have high sensitivity and selectivity for HIV.

The improved peptides have increased stability which allows the

peptides to react more favourably to give more sensitive tests. AAV79763

to AAV79868 represent peptides used in the exemplification of the

present invention.

Sequence 16 AA:

Query Match 76.4%; Score 68; DB 21; Length 16;

Best Local Similarity 73.3%; Pred. NO. 0.0012;

Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 LNSWCKGRICYS 15

1 : ||||| : |||||

Db 1 LNSWCKADROVCYTS 15

1 : ||||| : |||||

RESULT 25

AAV67608

AAV67608 standard; peptide: 17 AA.

AAV67608;

23-MAR-2000 (first entry)

Peptide #8 for detecting HIV-1 group O infection.

Human immunodeficiency virus-1; HIV-1; gp41 envelope protein; detection;

increased structural stability; diagnostic antigen.

Synthetic.

Key Location/Qualifiers

Misc-difference 4


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FT      /note- "mutated from Ser residue in wild type
FT      sequence (AAW16382)"
FT      Misc-difference 18
FT      /note- "mutated from Thr residue in wild type
FT      sequence (AAW16382)"
XX      WO9640763-A2.
XX      19-DEC-1996.
XX      07-JUN-1996: 96WO-US09655.
XX      07-JUN-1995: 95US-0472597.
XX      (ABBO ) ABBOTT LAB.
XX      Bridon DP, Colplits TL, Daghfal DJ, Jaffe KD, Size IS,
XX      WPI: 1997-052229/05.
XX      Hybrid polypeptide(s) comprising HIV-1 sub-type B immuno:dominant
XX      region - contg. 1 or more specific amino acid substitutions critical
XX      for detecting HIV-1 sub-type O, useful in immunoassay for detecting
XX      HIV antibodies
XX      Claim 12; Page 25; 34pp: English.
XX      The polypeptides AAW16379-81 represent peptides having point mutations
XX      in the HIV-1 sub-type B immunodominant region (IDR) at positions 604
XX      and/or 610. The peptides correspond to residues 593-611 of the gp41
XX      protein. This peptide has point mutations at positions 604 and 610. The
XX      invention relates to polypeptides which are hybrid polypeptides
XX      comprising the gp41 IDR of HIV-1 sub-type B contg. 1 or more specific
XX      amino acid substitutions critical for the detection of HIV-1 sub-type O.
XX      The polypeptides can be used for the detection of HIV antibodies.
XX      Sequence 19 AA:
SQ
Query Match      76.4%; Score 68; DB 18; Length 19;
Best Local Similarity 71.4%; Pred. No. 0.0014;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY      1 LNSWGCKGRITCYT 14
        | | | | | | | | | |
        6 LGIMGCKGKLCIYCT 19
Db
RESULT 28
AAV79853
ID      AAV79853 standard; Peptide: 16 AA.
XX
XX      AAV79853;
XX
XX      10-MAY-2000 (first entry)
XX
XX      HIV infection detection peptide SEQ ID NO:91.
XX
XX      Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;
XX      viral chimeric peptide; therapy; immunological.
XX
XX      Unidentified.
XX
XX      WO200001719-A2.
XX
XX      13-JAN-2000.
XX
XX      02-JUL-1999; 99WO-US15114.
XX
XX      02-JUL-1998; 98US-0091659.
XX      16-OCT-1998; 98US-0104685.
XX      11-DEC-1998; 98US-0112026.
XX
XX      (PEPT-) PEPTIDE SOLUTIONS.
XX

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XX      Chowdhury AM, Bernstein D, Kozhich A, Molsenbocker M;
XX      WPI: 2000-171000/15.
XX
XX      Novel viral-derived peptides used for the detection of human
XX      immunodeficiency virus (HIV) infection, particularly HIV-2 infection
XX      Disclosure; Fig 1; 67pp: English.
XX
XX      The present invention describes a peptide (I) for detecting HIV-2
XX      infection, which comprises a core Varicella-zoster protein 51 sequence.
XX      also described in the present invention are methods for detecting HIV
XX      infection. Peptides from the present invention can be used for the
XX      immunological detection of anti-HIV antibody, particularly for HIV-2
XX      testing. The peptides have high sensitivity and selectivity for HIV.
XX      The improved peptides have increased stability which allows the
XX      peptides to react more favourably to give more sensitive tests. AAV79763
XX      to AAV79868 represent peptides used in the exemplification of the
XX      present invention.
XX      Sequence 16 AA:
SQ
Query Match      75.3%; Score 67; DB 21; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.0017;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY      1 LNSWGCKGRITCYTS 15
        | | | | | | | | | |
        1 LNPWGCKAGKQVCYTS 15
Db
RESULT 29
AAV79844
ID      AAV79844 standard; Peptide: 16 AA.
XX
XX      AAV79844;
XX
XX      10-MAY-2000 (first entry)
XX
XX      HIV infection detection peptide SEQ ID NO:82.
XX
XX      Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;
XX      viral chimeric peptide; therapy; immunological.
XX
XX      Unidentified.
XX
XX      WO200001719-A2.
XX
XX      13-JAN-2000.
XX
XX      02-JUL-1999; 99WO-US15114.
XX
XX      02-JUL-1998; 98US-0091659.
XX      16-OCT-1998; 98US-0104685.
XX      11-DEC-1998; 98US-0112026.
XX
XX      (PEPT-) PEPTIDE SOLUTIONS.
XX
XX      Chowdhury AM, Bernstein D, Kozhich A, Molsenbocker M;
XX      WPI: 2000-171000/15.
XX
XX      Novel viral-derived peptides used for the detection of human
XX      immunodeficiency virus (HIV) infection, particularly HIV-2 infection
XX      Disclosure; Fig 1; 67pp: English.
XX
XX      The present invention describes a peptide (I) for detecting HIV-2
XX      infection, which comprises a core Varicella-zoster protein 51 sequence.
XX      also described in the present invention are methods for detecting HIV
XX      infection. Peptides from the present invention can be used for the
XX      immunological detection of anti-HIV antibody, particularly for HIV-2
XX

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testing. The peptides have high sensitivity and selectivity for HIV.
 CC The improved peptides have increased stability which allows the
 CC peptides to react more favourably to give more sensitive tests. AAY79763
 CC to AAY79868 represent peptides used in the exemplification of the
 CC present invention.

XX Sequence 16 AA;

Query Match 74.2%; Score 66; DB 21; Length 16;
 Best Local Similarity 66.7%; Pred. No. 0.0024;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 LNSGCKGRILICYTS 15
 ||:|||||:|||||
 Db 1 LNAMGCANROVCYTS 15

RESULT 30

AAY79843 standard; Peptide: 16 AA.

XX AAY79843;

XX 10-MAY-2000 (first entry)

DE HIV infection detection peptide SEQ ID NO:81.

XX Varicella zoster virus; HIV; HIV-2; detection; diagnosis; infection;
 KW viral chimeric peptide; therapy; immunological.

XX Unidentified.

FN WO200001719-A2.

XX 13-JAN-2000.

XX 02-JUL-1999; 99WO-US15114.

XX 02-JUL-1998; 98US-0091659.

PR 16-OCT-1998; 98US-0104685.

PR 11-DEC-1998; 98US-0112026.

XX (PEPT-) PEPTIDE SOLUTIONS.

XX Chowdhury AM, Bernstein D, Kozhich A, Molsenbocker M;

XX WPI; 2000-171000/15.

XX Novel viral-derived peptides used for the detection of human
 PT immunodeficiency virus (HIV) infection, particularly HIV-2 infection
 XX Disclosure; Fig 1; 67pp; English.

XX The present invention describes a peptide (I) for detecting HIV-2
 CC infection, which comprises a core Varicella-Zoster protein 51 sequence.
 CC also described in the present invention are methods for detecting HIV
 CC infection. Peptides from the present invention can be used for the
 CC immunological detection of anti-HIV antibody, particularly for HIV-2
 CC testing. The peptides have high sensitivity and selectivity for HIV.
 CC The improved peptides have increased stability which allows the
 CC peptides to react more favourably to give more sensitive tests. AAY79763
 CC to AAY79868 represent peptides used in the exemplification of the
 CC present invention.

XX Sequence 16 AA;

Query Match 73.0%; Score 65; DB 21; Length 16;
 Best Local Similarity 66.7%; Pred. No. 0.0034;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 LNSGCKGRILICYTS 15
 ||:|||||:|||||
 Db 1 LNAMGCANROVCYTS 15

Search completed: June 5, 2003, 08:59:22
 Job time : 35 secs